


```

967 6 0.8 351 2 09288 09218 neisseria m
968 6 0.8 351 2 02354 02354 leishmania
969 6 0.8 351 2 02354 02354 leishmania
970 6 0.8 351 10 04250 04250 arabidopsis
971 6 0.8 351 12 069284 069284 turkay hept
972 6 0.8 352 2 09916 09916 neisseria m
973 6 0.8 352 2 09916 09916 neisseria m
974 6 0.8 352 2 09916 09916 neisseria m
975 6 0.8 353 1 030166 030166 arabidopsis
976 6 0.8 353 10 099822 099822 arabidopsis
977 6 0.8 354 2 051258 051258 neisseria m
978 6 0.8 354 2 051258 051258 neisseria m
979 6 0.8 354 2 051258 051258 neisseria m
980 6 0.8 354 2 051258 051258 neisseria m
981 6 0.8 354 2 051258 051258 neisseria m
982 6 0.8 354 2 051258 051258 neisseria m
983 6 0.8 354 2 051258 051258 neisseria m
984 6 0.8 354 12 067629 067629 arabidopsis
985 6 0.8 355 2 056598 056598 arabidopsis
986 6 0.8 355 2 056598 056598 arabidopsis
987 6 0.8 355 2 056598 056598 arabidopsis
988 6 0.8 355 2 056598 056598 arabidopsis
989 6 0.8 355 2 056598 056598 arabidopsis
990 6 0.8 355 2 056598 056598 arabidopsis
991 6 0.8 355 2 056598 056598 arabidopsis
992 6 0.8 356 2 09916 09916 neisseria m
993 6 0.8 356 2 09916 09916 neisseria m
994 6 0.8 356 2 09916 09916 neisseria m
995 6 0.8 356 2 09916 09916 neisseria m
996 6 0.8 357 1 059046 059046 arabidopsis
997 6 0.8 357 2 051203 051203 neisseria m
998 6 0.8 357 2 051203 051203 neisseria m
999 6 0.8 357 2 051203 051203 neisseria m
1000 6 0.8 357 2 051203 051203 neisseria m

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ALIGNMENTS

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RESULT 1
ID 043748 PRELIMINARY: PRT: 750 AA.
AC 043748
DT 01-JUN-1998 (TREMBL) 06: Created
DR 01-OCT-2000 (TREMBL) 15: Last sequence update
DR 01-OCT-2000 (TREMBL) 15: Last annotation update
DE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
GN PSM
OC Homo sapiens (human)
OS Homo sapiens (human)
RA Hsuang-Yi, Chen, Choudhary, Crenshaw, Verheul, Euteneier,
OC Mammalia: Euteleostomi: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Euteleostomi: Chordata: Craniata: Vertebrata: Euteleostomi:

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DB 556 YETTELVERPPEKTLVAVGNGCHVTELANSTVPPGCHVAVLAKADITISIS 615
DB 572 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 631
DB 616 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 675
DB 632 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 691
DB 676 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 735
DB 692 AFTVQAAETISRNA 706
DB 736 AFTVQAAETISRNA 750

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RESULT 2

```

ID 09915 PRELIMINARY: PRT: 110 AA.
AC 09915
DT 01-OCT-2000 (TREMBL) 15: Created
DR 01-OCT-2000 (TREMBL) 15: Last sequence update
DR 01-OCT-2000 (TREMBL) 15: Last annotation update
DE PROSTATE-SPECIFIC MEMBRANE ANTIGEN PSM (PROSTATE)
OS Homo sapiens (human)
RA Hsuang-Yi, Chen, Choudhary, Crenshaw, Verheul, Euteneier,
OC Mammalia: Euteleostomi: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Euteleostomi: Chordata: Craniata: Vertebrata: Euteleostomi:

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DB 556 YETTELVERPPEKTLVAVGNGCHVTELANSTVPPGCHVAVLAKADITISIS 615
DB 572 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 631
DB 616 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 675
DB 632 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 691
DB 676 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 735
DB 692 AFTVQAAETISRNA 706
DB 736 AFTVQAAETISRNA 750

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DB 556 YETTELVERPPEKTLVAVGNGCHVTELANSTVPPGCHVAVLAKADITISIS 615
DB 572 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 631
DB 616 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 675
DB 632 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 691
DB 676 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 735
DB 692 AFTVQAAETISRNA 706
DB 736 AFTVQAAETISRNA 750

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Query Match 10.1% Score 71: DB 4: Length 110:
Best Local Similarity 100.0% Pred. No 5: 8e-67
Matches 71: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
542 ELANSIVLPDCHGAVLAKADITISISMKRDKQNTVSPDLSAVNPTETAS 601

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DB 556 YETTELVERPPEKTLVAVGNGCHVTELANSTVPPGCHVAVLAKADITISIS 615
DB 572 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 631
DB 616 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 675
DB 632 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 691
DB 676 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 735
DB 692 AFTVQAAETISRNA 706
DB 736 AFTVQAAETISRNA 750

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Query Match 95.6% Score 675: DB 4: Length 750:
Best Local Similarity 100.0% Pred. No 0:
Matches 675: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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DB 556 YETTELVERPPEKTLVAVGNGCHVTELANSTVPPGCHVAVLAKADITISIS 615
DB 572 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 631
DB 616 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 675
DB 632 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 691
DB 676 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 735
DB 692 AFTVQAAETISRNA 706
DB 736 AFTVQAAETISRNA 750

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DB 556 YETTELVERPPEKTLVAVGNGCHVTELANSTVPPGCHVAVLAKADITISIS 615
DB 572 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 631
DB 616 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 675
DB 632 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 691
DB 676 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 735
DB 692 AFTVQAAETISRNA 706
DB 736 AFTVQAAETISRNA 750

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RESULT 3

```

ID 09915 PRELIMINARY: PRT: 84 AA.
AC 09915
DT 01-OCT-2000 (TREMBL) 15: Created
DR 01-OCT-2000 (TREMBL) 15: Last sequence update
DR 01-OCT-2000 (TREMBL) 15: Last annotation update
DE PROSTATE-SPECIFIC MEMBRANE ANTIGEN PSM (PROSTATE)
OS Homo sapiens (human)
RA Hsuang-Yi, Chen, Choudhary, Crenshaw, Verheul, Euteneier,
OC Mammalia: Euteleostomi: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Euteleostomi: Chordata: Craniata: Vertebrata: Euteleostomi:

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DB 556 YETTELVERPPEKTLVAVGNGCHVTELANSTVPPGCHVAVLAKADITISIS 615
DB 572 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 631
DB 616 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 675
DB 632 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 691
DB 676 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 735
DB 692 AFTVQAAETISRNA 706
DB 736 AFTVQAAETISRNA 750

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DB 556 YETTELVERPPEKTLVAVGNGCHVTELANSTVPPGCHVAVLAKADITISIS 615
DB 572 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 631
DB 616 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 675
DB 632 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 691
DB 676 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 735
DB 692 AFTVQAAETISRNA 706
DB 736 AFTVQAAETISRNA 750

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```

DB 556 YETTELVERPPEKTLVAVGNGCHVTELANSTVPPGCHVAVLAKADITISIS 615
DB 572 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 631
DB 616 KAPQDKETVSPDLSAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 675
DB 632 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 691
DB 676 IDPLDLPDPPEHNTVYANSSNNTVAGSSPQITDLDLISAVDPSTKNGEYKQIYA 735
DB 692 AFTVQAAETISRNA 706
DB 736 AFTVQAAETISRNA 750

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Query Match 7.6% Score 54: DB 4: Length 84:
Best Local Similarity 100.0% Pred. No 5: 1e-46
Matches 54: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
116 PPSAVPQCHPQDOLVYVAVNPTETASPERLDDPKSNPTVLANHNDQALPRLAP 169

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RP SEQUENCE FROM N.A.
RX TISSUE=J:STJNAL.MUSCUL.
RL MEDLINE=68552022; PubMed=6663535;
RA "Ling B., Lohm-Carter R., Villanueva J.A., Gardner J.M.,
RA Goble C.T.,"
RT "Poly[gamma-glutamate carboxypeptidase from pig jejunum.
RT Molecular characterization and relation to glutamate carboxypeptidase
RT J Biol. Chem. 273:20417-20424(1998).
DR EMBL: AF050502; M393269.1; -.
DR GENBANK: AF050502.1; -.
DR INTERPRO: IPR003137; -.
DR PROSITE: PS00136; 1.
DR CARBOXYPEPTIDASE 1.
SQ SEQUENCE 751 AA; 8453 MW; AF7B532638BCA CRC64;

Query Match 7.19; Score 50; DB 6; Length 751;
Reef Local Similarity 100.0%; Pred. No. 7+e-44;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 310 RIVYVGTGTCAGVPEPVYVTCGHSRQVPCIDPGSCAAVHYEIVSRG 359
DB 355 RIVYVGTGTCAGVPEPVYVTCGHSRQVPCIDPGSCAAVHYEIVSRG 404

ID 035409 PRELIMINARY; PRT; 752 AA.
AC 035409
DT 01-JUN-1998 (REDBIOL 05; Created)
DR 01-OCT-2000 (REDBIOL 15; Sequence update)
DR 01-OCT-2000 (REDBIOL 15; Last annotation update)
DE PROSTATE-SPECIFIC MEMBRANE ANTIGEN HOMOLOG.
GN PSMA OR NPSM.
OS Mus musculus (mouse).
OC Chordata; Chariata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxId=10090;
RN 1(1)
RS SEQUENCE FROM N.A.
RX TISSUE=J:STJNAL.MUSCUL.
RL MEDLINE=68552022; PubMed=6663535;
RA "Ling B., Lohm-Carter R., Villanueva J.A., Gardner J.M.,
RA Goble C.T.,"
RT "Poly[gamma-glutamate carboxypeptidase from pig jejunum.
RT Molecular characterization and relation to glutamate carboxypeptidase
RT J Biol. Chem. 273:20417-20424(1998).
DR EMBL: AF050502; M393269.1; -.
DR GENBANK: AF050502.1; -.
DR INTERPRO: IPR003137; -.
DR PROSITE: PS00136; 1.
DR CARBOXYPEPTIDASE 1.
SQ SEQUENCE 752 AA; 8463 MW; DB8F71094E4A50926A CRC64;

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Query Match          5.1% Score 36; DB 11; Length 752;
Best Local Similarity 100.0%; Pred. No.5e-29;
Matches   36; Conservative 0; Mismatches 0; Gaps
                                0; Indels      0; Gaps
Cy    359 SRLLQSRVAVTINNDSSICHTATDAPGPGMAYV 430
Db    441 SRLLQSRVAVTINNDSSICHTATDAPGPGMAYV 476

RESULT      6
P07627 ID P07627 PRELIMINARY: PRT: 752 AA.
DC AT     0-FRR-1997 (REBIOBEL_07_Created)
DT DT     01-OCT-2000 (REBIOBEL_07_Created)
DT DT     01-OCT-2000 (REBIOBEL_15_Last annotation update)
DE NAC-Peptidase (GLUTAMATE CARBOXYPEPTIDASE II) [EC 3.4.17.21].
OC Rattus norvegicus (Rat); Canis familiaris (Dog);
OC Mus musculus (Mouse); Chondria; Gallus gallus (Chicken);
OC Balaenoptera musculus (Humpback whale); Scutigera coleopator (Centipede); Rattus
OX NCBI_TaxId=10116;
NM NM [1]
RP SEQUENCE FROM N.A.
RC STRIPING-BRAIN-TISSUE-RNAIY; TISUS-BRAIN;
RC STRIPING-BRAIN-TISSUE-RNAIX; TISUS-BRAINX;
RA Bridge T., Turri T., Wroblewska B., She D., Chung H.S., Kim R.,
RA Neale J.H.;
FT "Molecular cloning of a peptidase against N-acetylserpinolytic
FT cleavage site."
RM PubMed 89-2270-2277(1997)
[2]
RP SEQUENCE FROM N.A.
RC TISUS-BRAIN-TISSUE-RNAIY; Peptidase-9501241;
RC TISUS-BRAIN-TISSUE-RNAX; Peptidase-9501241;
RA Luthi-Carter R., Berger U.V., Barakat A.K., Enns M., Coyle J.T.;
FT "Isolation and expression of a rat brain cDNA encoding glutamate
FT carboxypeptidase II."
RM Proc. Natl. Acad. Sci. U.S.A. 95:3215-3220(1998).
RL
RP SEQUENCE OF 384-752 FROM N.A.
RC MEDLINR-96149377; Pubmed=9570628;
RX MEDLINR-96149377; Pubmed=9570628;
RA Carlsberg C., Kjaer S., Thomsen M., Jensen T.J.;
RA "Characterization of a specific membrane antigen as a hydrolase with substrate and
RA pharmacological characteristics of a neutrophilic *."
RM Proc. Natl. Acad. Sci. U.S.A. 93:7479-753(1996).
[4]
RP SEQUENCE OF 384-752 FROM N.A.
RC TISUS-BRAIN;
RA Luthi-Carter R., Berger U.V., Barakat A.K., Enns M., Coyle J.T.;

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un -08-403-803-2_copy45_750-011g-trspt
Apr 9 11:16:16 2001

BL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: 075973; AAC54433.1;
DR EMBL: AF040356; AAC40067.1;
DR EMBL: AF038701; AAC56739.1;
DR EMBL: AF040356; AAC40067.1;
DR INTERPRO: IPR001337;
DR PIRAM: P00225; PA.1;
DR Carboxypeptidase: Hydrolase.
DS SEQUENCE 752 AA: 84539 MW: 50915339671261 CRCK4.

Query Match
Beat Local Similarity 100.0%; Score 34; DB 11; Length 752;
Matches 34; Consecutive 0; Mismatches 0; Indels 0; Gaps 0

QY 464 CHNRISLGSNDSEVFQRIQLNSGRATYNN 497
DB 510 CHNRISLGSNDSEVFQRIQLNSGRATYNN 543
|||||
|||||

RESULT 7
ID QY3Y30 PRELIMINARY; PRT; 740 AA.
ID QY3Y30
DT 01-NOV-1999 (TRERELE); 12. Created
DT 01-MOV-1999 (TRERELE); 12. Last sequence update
DT 01-OCT-2000 (TRERELE); 15. Last annotation update
DR MALLAKONE II PROTEIN.
DE Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo
OC Hominidae; Homininae;
OC NCBI_Taxid=9606;
NCBI_Taxid=9606;
SEQUENCE FROM N.A.
RP TISSUE=JUNG CARCINOMA.
RX MEDLINE=93145063; PubMed=10035073;
RX Gordon R.G., Neils D.H., Somers N., Freilones E., Ashton D.,
RX Isolation and expression of novel human glutamate carboxypeptidases
RX with N-acetylated alpha-linked aspartic dipeptides and dipeptidyl
RX peptidase IV activity (DB:048131999).
DR EMBL: A002370; CAB399671.1;
DR MEROSES; M8 012;
DS SEQUENCE 740 AA: 83591 MW: 040624059182CP873 CRCK4.

Query Match
Beat Local Similarity 100.0%; Score 24; DB 4; Length 740;
Matches 24; Consecutive 0; Mismatches 0; Indels 0; Gaps 0

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un-08-403-803-2.ccopy_45_750.o19.i.p
Nov Apr 9 11:14:16 2001

QY      123 GGGPGGGLLVVNVNATFEDFFKLR 146
       | | | | | | | | | | | | | | | | | |
Db      157 GGGPGGGLVVVNATFEDFFKLR 180

RESULT   8
CD        0
ID        0 LE305          PRELIMINARY:    PRT:    29 AA.
AC        0 LE305
DT        0 01-NOV-1996 (TIBREBEL: 01_Created)
DE        0 PROSTATE-SPECIFIC MEMBRANE ANTIGEN UPDATE)
DT        0 01-NOV-2000 (TIBREBEL: 15_Last annotation update)
OS        0 Prostate-specific membrane antigen (PROAGENT).
OC        Homo sapiens (HUMAN).
CN        Enayazyga Metastomus; chordata; Craniata; Vertebrata; Euteleostomi;
           Osteichthyes; Actinopterygii; Clariidae; Catfishes; Hemibarbus; Hemib
           MC1_Tetraodon666.
RN         11
RP        SEQUENCE FROM N.A.
RC        TISSUE=PROSTATE; PubMed=7882349;
RZ        Su S.L., Huang I.P., Fair M.R., Powell C.T., Heston W.D.;
RT        "Alternatively spliced variants of prostate-specific membrane antigen
RL        RNA: ratio of expression as a potential measurement of progression";
RI        Cancer Res. 55:1441-1443(1995);
RJ        NCBI=68706; DBS=J01592.
PT        NON_FER
SO        SEQUENCE     29 AA: 3455 HW: 1B2GBEAF63867D2 CRC64:

Query March               3 0% Score 21: DB 4: Length 29;
Best Local Similarity 100.0%; Pred.No. 2.e+14;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Caps

QY      22 KAKIKKEFYVFOIPIHACT 42
       | | | | | | | | | | | | | | | | | |
Db      9 KAKIKKEFYVFOIPIHACT 29

RESULT   9
CD        0
ID        0 Q9HQO1          PRELIMINARY:    PRT:    740 AA.
AC        0 Q9HQO1
DT        0 01-MAY-2000 (TIBREBEL: 13_Created)
DE        0 Proteinase 1 (Proteinase 1, Last annotation update)
DT        0 01-OCT-2000 (TIBREBEL: 15_Last annotation update)
DE        WKALADASE L. PROTEIN.
CN        WKALADASE L.
OC        Homo sapientia (Human).
CN        Bathyraja; Metaceta; Chordata; Vertebrata; Euteleostomi;
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CC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OC	NCBI_TaxID:9606;
RA	SEQUENCE FROM R.A.
RC	TISSUE=SKIN; TISSUE=SMALL INTESTINE;
BA	Pargalos M.N., Necs J.M., Somers M., Fraiponts E., Ashton D.,
GT	Gordon R.G.,
RT	with N-acetylated alpha-linked acidic dipeptidase and dipeptidyl
AT	peptidase IV activity.
RL	J. Biol. Chem. 274:8470-8481(1999).
DR	INTERPRO: IP000719; Pfam0137; -
DR	INTERPRO: IP0003137; -
DR	PFAM: PF02325; PA: 1.
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1
DR	SMART: SMO026; 140 AA; 60020 MW; E2B5AC35056A14 CIRC64;
Query Match	1.4%; Score 10; DB 4; Length 740;
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	319 RQWERYRY 328
Db	354 RQWERYRY 363
RESULT 10	
ID	054697
AC	054697;
DT	01-JUN-1998 (FBIHrel_06, Created)
DR	01-OCT-2000 (FBIHrel_15, Last annotation update)
DE	1100.
OS	Rattus norvegicus (Rat).
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RA	Bayerlato, Metzger, Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID:10116;	
[1]	
SEQUENCE FROM R.A.	
RA	Shneider B.L., Thevanathar S., Meyer M.S., Walters R.C., Rinaldo P.,
RA	Devasthan J.P., Sun A.O., Davson P.A., Ananthanaryanan M.,
RL	J. Biol. Chem. 0:0-0(1997).
DR	MEMOS: 3429.011; AAB87644.1; -
DR	INTERPRO: IP0003137; -
DR	PFAM: PF02325; PA: 1
SEQUENCE 745 AA; 80640 MW; A59C2EFD23BE31695 CIRC64;	

[illegible]

RESULT 12
 09M188
 ID 01M188
 AD 01M188
 PR PRELIMINARY: PRT: 703 AA.
 DT 01-OCT-2000 (TREMBL: 15, Created)
 DT 01-OCT-2000 (TREMBL: 15, Last sequence update)
 DT 01-OCT-2000 (TREMBL: 15, Last annotation update)
 GN 1523
 GN 75M23.86: LINE PROTEIN.
 OS Arabidopsis thaliana (House-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliopsida; eudicots; Rosales; Rosidae; eucroside II;
 OC NCBI_taxid:54045; Malvaceae; Malvaceae.
 ON NCBI_taxid:3702;
 ON (1)
 BR SEQUENCE FROM N.A.
 RP Dr. David P. F. X. Querretes, Dr. Patricia K., Steiner H. M.,
 RP Lemke R., Meyer P. F. X., Querretes, Dr. Patricia K., Steiner H. M.,
 RL Submitted (FEB-2000) to the EMBD/GenBank/DBJ databases.
 BR (2)
 BR SEQUENCE FROM N.A. financing project.
 RP Dr. David P. F. X. Querretes, Dr. Patricia K., Steiner H. M.,
 RL Submitted (MAR-2000) to the EMBD/GenBank/DBJ databases.
 DBE1: AL138650; CAB7592.1; ..
 QD SEQUENCE 703 AA: 76925 MW: 288140PFLIK4B204 CRC64;

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Query Match      1.3%   Score 9;   DB 10;   Length 703;
Best Local Similarity 100.0%;   Pred. No. 2.5;
Matches          0;   Mismatches          0;   Gaps          0
OY              365 GMPRTTIL 373
                |||||
Db               388 GMPRTTIL 396

RESULT 13
OY              GAYVUD
AC              PRELIMINARY;    PRT; 1306 AA.
GAYVUD;
D7 01-MAY-1999 (FEBMAREL_10_Created)
D7 01-MAY-1999 (FEBMAREL_10_Last sequence update)
D7 01-MAY-1999 (FEBMAREL_10_Protein length updated)
DE ORF NSV152 POSITIVE CORE PROTEIN PAA HOMOLOGS (VACCINIA A10L), SIMILAR
DE TO SM:P31817.
OR NSV152.
OR NSV152 HAS ANALOGUES entomopoxvirinae
OC Viruses::dsDNA viruses, no RNA stage: Poxviridae; Entomopoxvirinae;
OC Entomopoxvirinae B.
NCBI_TaxID=81391.
OX
```


SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA.
RA Waterston R.
RN 16
RP Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
RP SEQUENCE FROM N.A.
RA EV Arabidopsis sequencing project:
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RC EMBL: AB024211.1
DR EMBL: AB024211.1
SQ SEQUENCE 280 AA: 3115 MW: AB/ECF4E187036 CRC64:

Query Match
Best Local Similarity 100.0%; Score 8; DB 10; Length 280;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 323 EPPRVITL 330
DB 176 EPPRVITL 183

RESULT 20
ID 09LCJ3 PRELIMINARY: PRT: 303 AA.
AC 09LCJ3
DT 01-OCT-2000 (TRIMBLrel. 15, Created)
DT 01-OCT-2000 (TRIMBLrel. 15, Last sequence update)
DE NA-TRANSLOCATING NADH-QUINONE REDUCTASE (FRAGMENT).
OS Arabidopsis thaliana.
OC Eukaryota; Eukaryota; Eukaryota; gamma subunit; Alteromonadaceae;
OC Alteromonas.
OC NCBI_TaxID=28108;
RN SEQUENCE FROM N.A.
RA Kato S., Yumoto I.;
RT Detection and distribution of Na-translocating NADH-quinone reductase
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB024211.1; BAA83758.1;
FT NON_TER 1 1
SQ SEQUENCE 303 AA: 34905 MW: 56CD25C85931131 CRC64:

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 303;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 393 ENRNLOE 400
DB 145 ENRNLOE 152

RESULT 22
ID 01382 PRELIMINARY: PRT: 694 AA.
AC 01382
DT 01-JUN-1998 (TRIMBLrel. 05, Created)
DT 01-JUN-1998 (TRIMBLrel. 05, Last sequence update)
DE 01-MAY-2000 (TRIMBLrel. 15, Last annotation update)
OS Arabidopsis thaliana.
OC Eukaryota; Eukaryota; Eukaryota; gamma subunit; Alteromonadaceae;
OC Alteromonas.
OC NCBI_TaxID=28108;
RN SEQUENCE FROM N.A.
RA Borer D.H., Klinger J.R.,
RT Detection and distribution of Na-translocating NADH-quinone reductase
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB024211.1; BAA83758.1;
FT NON_TER 1 1
SQ SEQUENCE 303 AA: 34905 MW: 56CD25C85931131 CRC64:

Query Match
Best Local Similarity 100.0%; Score 8; DB 3; Length 694;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 260 MERNKGC 267
DB 673 KILERNKGC 680

RESULT 23
ID P91406 PRELIMINARY: PRT: 751 AA.
AC P91406
DT 01-OCT-1997 (TRIMBLrel. 03, Created)
DT 01-OCT-1997 (TRIMBLrel. 03, Last sequence update)
DE SIMILAR TO HUMAN PROSTATE-SPECIFIC MEMBRANE ANTIGEN.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Chordata; Rhododactyla; Rhododactylidae;
OC NCBI_TaxID=6239;
RN SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;

CY 669 FDIERNK 676
DB 126 FDIERNK 133

RESULT 21
ID 09NSM7 PRELIMINARY: PRT: 549 AA.
AC 09NSM7
DT 01-OCT-2000 (TRIMBLrel. 15, Created)
DT 01-OCT-2000 (TRIMBLrel. 15, Last sequence update)
DE HYPOTHETICAL PROTEIN H2113.3.
OS Caenorhabditis elegans.
OC Eukaryota; Eukaryota; Eukaryota; gamma subunit; Alteromonadaceae;
OC Alteromonas.
OC NCBI_TaxID=6239;
RN SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RT The sequence of C. elegans conid H2113.3.
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
RN 11
SQ SEQUENCE FROM N.A.
RA Waterston R.;
RT Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AC006856.1; AA33882.1;
SQ SEQUENCE 549 AA: 65212 MW: B600875A571E238 CRC64:

Query Match
Best Local Similarity 100.0%; Score 8; DB 5; Length 549;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 393 ENRNLOE 400
DB 145 ENRNLOE 152

RESULT 24
ID 09NLE4 PRELIMINARY: PRT: 989 AA.
AC 09NLE4
DT 01-OCT-2000 (TRIMBLrel. 15, Created)
DT 01-OCT-2000 (TRIMBLrel. 15, Last sequence update)
OS Arabidopsis thaliana.
OC Eukaryota; Eukaryota; Eukaryota; gamma subunit; Alteromonadaceae;
OC Alteromonas.
OC NCBI_TaxID=28108;
RN SEQUENCE FROM N.A.
RA Kato S., Yumoto I.;
RT Detection and distribution of Na-translocating NADH-quinone reductase
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB024211.1; BAA83758.1;
FT NON_TER 1 1
SQ SEQUENCE 303 AA: 34905 MW: 56CD25C85931131 CRC64:

RESULT 25
ID 09NLE4 PRELIMINARY: PRT: 989 AA.
AC 09NLE4
DT 01-OCT-2000 (TRIMBLrel. 15, Created)
DT 01-OCT-2000 (TRIMBLrel. 15, Last sequence update)
OS Arabidopsis thaliana.
OC Eukaryota; Eukaryota; Eukaryota; gamma subunit; Alteromonadaceae;
OC Alteromonas.
OC NCBI_TaxID=28108;
RN SEQUENCE FROM N.A.
RA Kato S., Yumoto I.;
RT Detection and distribution of Na-translocating NADH-quinone reductase
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB024211.1; BAA83758.1;
FT NON_TER 1 1
SQ SEQUENCE 303 AA: 34905 MW: 56CD25C85931131 CRC64:

Query Match
Best Local Similarity 100.0%; Score 8; DB 5; Length 989;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 377 MERNKGC 384
DB 413 MERNKGC 420

RESULT 26
ID 09NLE4 PRELIMINARY: PRT: 989 AA.
AC 09NLE4
DT 01-OCT-2000 (TRIMBLrel. 15, Created)
DT 01-OCT-2000 (TRIMBLrel. 15, Last sequence update)
OS Arabidopsis thaliana.
OC Eukaryota; Eukaryota; Eukaryota; gamma subunit; Alteromonadaceae;
OC Alteromonas.
OC NCBI_TaxID=28108;
RN SEQUENCE FROM N.A.
RA Kato S., Yumoto I.;
RT Detection and distribution of Na-translocating NADH-quinone reductase
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB024211.1; BAA83758.1;
FT NON_TER 1 1
SQ SEQUENCE 303 AA: 34905 MW: 56CD25C85931131 CRC64:

PROSITE: PRO0453: PRP_PRIASE.1.1.
 DR PROSITE: PRO0454: PRP_PRIASE.2.1.
 DR PROSITE: PRO0459: PRP_PRIASE.3.1.
 KM Iemestrace.
 SQ SEQUENCE 152 AA: 16591 MW: 40035319855908 CRC64:

Query Match 1.0%: Score 7; DB 2; Length 152;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 487 ASGNARY 493
 DB 34 ASGNARY 40
 |||||

RESULT 34
 ID Q59306 PRELIMINARY: PRT: 165 AA.

AC Q59306
 DT 01-OCT-2000 (TRFBIrel. 15; Created)
 DT 01-OCT-2000 (TRFBIrel. 15; Last sequence update)
 DT 01-OCT-2000 (TRFBIrel. 15; Last annotation update)
 DR PROSITE: PRO0453: PRP_PRIASE.1.1.
 DR PROSITE: PRO0454: PRP_PRIASE.2.1.
 DR PROSITE: PRO0459: PRP_PRIASE.3.1.
 KM Iemestrace.
 SQ SEQUENCE 152 AA: 16591 MW: 40035319855908 CRC64:
 OC Bacillus halodurans.
 OC Bacteria: Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Clostridium group; Bacillus.
 OC Bacillus/Clostridium group; Bacillus.
 RN [1] _L:taxid=9606;
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 6136169; PubMed: 6026330;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB001516; BAB06308.1; -
 SQ SEQUENCE 165 AA: 18304 MW: 2839DF19064D051 CRC64:

Query Match 1.0%: Score 7; DB 2; Length 165;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 110 VSDIYPP 116
 DB 142 VSDIYPP 148
 |||||

RESULT 35
 ID Q59B33 PRELIMINARY: PRT: 173 AA.

AC Q59B33
 DT 01-NOV-1996 (TRFBIrel. 01; Created)
 DT 01-NOV-1996 (TRFBIrel. 01; Last sequence update)
 DR PROSITE: PRO0453: PRP_PRIASE.1.1.
 DR PROSITE: PRO0454: PRP_PRIASE.2.1.
 DR PROSITE: PRO0459: PRP_PRIASE.3.1.
 KM Iemestrace.
 SQ SEQUENCE 163 AA: 20120 MW: 1F2BPCD09928458 CRC64:
 OC Bacillus halodurans.
 OC Bacteria: Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Clostridium group; Bacillus.
 RN [1] _L:taxid=9606;
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 6136169; PubMed: 6026330;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB001516; BAB06308.1; -
 SQ SEQUENCE 165 AA: 18304 MW: 2839DF19064D051 CRC64:
 OC Bacillus halodurans.
 OC Bacteria: Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Clostridium group; Bacillus.
 RN [1] _L:taxid=9606;
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 6136169; PubMed: 6026330;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB001516; BAB06308.1; -
 SQ SEQUENCE 165 AA: 18304 MW: 2839DF19064D051 CRC64:

Query Match 1.0%: Score 7; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 24 ENIKFPL 30
 DB 120 ENIKFPL 126
 |||||

RESULT 37
 ID Q59373 PRELIMINARY: PRT: 183 AA.

AC Q59373
 DT 01-NOV-1996 (TRFBIrel. 01; Created)
 DT 01-NOV-1996 (TRFBIrel. 01; Last sequence update)
 DT 01-MAY-2000 (TRFBIrel. 13; Last annotation update)
 DR PROSITE: PRO0453: PRP_PRIASE.1.1.
 DR PROSITE: PRO0454: PRP_PRIASE.2.1.
 DR PROSITE: PRO0459: PRP_PRIASE.3.1.
 KM Iemestrace.
 SQ SEQUENCE 152 AA: 16591 MW: 40035319855908 CRC64:
 OC Bacillus halodurans.
 OC Bacteria: Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Clostridium group; Bacillus.
 RN [1] _L:taxid=9606;
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 6136169; PubMed: 6026330;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB001516; BAB06308.1; -
 SQ SEQUENCE 165 AA: 18304 MW: 2839DF19064D051 CRC64:

DT 01-NOV-1996 (TRFBIrel. 12; Created)
 DT 01-NOV-1996 (TRFBIrel. 12; Last sequence update)
 DT 01-MAY-2000 (TRFBIrel. 13; Last annotation update)
 DR PROSITE: PRO0453: PRP_PRIASE.1.1.
 DR PROSITE: PRO0454: PRP_PRIASE.2.1.
 DR PROSITE: PRO0459: PRP_PRIASE.3.1.
 KM Iemestrace.
 SQ SEQUENCE 152 AA: 16591 MW: 40035319855908 CRC64:

Query Match 1.0%: Score 7; DB 1; Length 173;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 604 ERLDPPD 610
 DB 72 ERLDPPD 78
 |||||

RESULT 36
 ID Q59391 PRELIMINARY: PRT: 183 AA.

AC Q59391
 DT 01-NOV-1996 (TRFBIrel. 01; Created)
 DT 01-NOV-1996 (TRFBIrel. 01; Last sequence update)
 DT 01-MAY-2000 (TRFBIrel. 13; Last annotation update)
 DR PROSITE: PRO0453: PRP_PRIASE.1.1.
 DR PROSITE: PRO0454: PRP_PRIASE.2.1.
 DR PROSITE: PRO0459: PRP_PRIASE.3.1.
 KM Iemestrace.
 SQ SEQUENCE 152 AA: 16591 MW: 40035319855908 CRC64:
 OC Bacillus halodurans.
 OC Bacteria: Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Clostridium group; Bacillus.
 RN [1] _L:taxid=9606;
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 6136169; PubMed: 6026330;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB001516; BAB06308.1; -
 SQ SEQUENCE 165 AA: 18304 MW: 2839DF19064D051 CRC64:

RT Complete DNA sequence and structural analysis of the enteropathogenic
 RT Enteropathogenic E. coli adherence factor plasmid.
 DR PROSITE: PRO0453: PRP_PRIASE.1.1.
 DR PROSITE: PRO0454: PRP_PRIASE.2.1.
 DR PROSITE: PRO0459: PRP_PRIASE.3.1.
 KM Iemestrace.
 SQ SEQUENCE 183 AA: 20148 MW: C871C0F022844A CRC64:

Query Match 1.0%: Score 7; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 24 ENIKFPL 30
 DB 120 ENIKFPL 126
 |||||

RESULT 38
 ID Q59A82 PRELIMINARY: PRT: 225 AA.

AC Q59A82
 DT 01-MAY-1999 (TRFBIrel. 10; Created)
 DT 01-MAY-1999 (TRFBIrel. 10; Last sequence update)
 DT 01-MAY-1999 (TRFBIrel. 10; Last annotation update)
 DR PROSITE: PRO0453: PRP_PRIASE.1.1.
 DR PROSITE: PRO0454: PRP_PRIASE.2.1.
 DR PROSITE: PRO0459: PRP_PRIASE.3.1.
 KM Iemestrace.
 SQ SEQUENCE 152 AA: 16591 MW: 40035319855908 CRC64:
 OC Bacillus halodurans.
 OC Bacteria: Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Clostridium group; Bacillus.
 RN [1] _L:taxid=9606;
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 6136169; PubMed: 6026330;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB001516; BAB06308.1; -
 SQ SEQUENCE 165 AA: 18304 MW: 2839DF19064D051 CRC64:


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D7 01-NOV-1998 (TRENDEL) 08 Last sequence update)
D8 01-NOV-1998 (TRENDEL) 08 Last annotation update)
D9 PROTEINOMIT TRANSLOCASE (TRAMERMY).
DN SECCA.
O5 Prochloron didemni.
OS Bacteriella cyanobacteria; Prochlorophytes; Prochlorococcus; Prochloron.
ON [1]
RN "Cambridge".
AP SEQUENCE FROM N.A.
RA Barbrook A.C.: unpublished (MAR-1999) to the EMBL/Jembay/DBS databases.
RN [1]
RP SEQUENCE FROM N.A.
RA Barbrook A.C.: University of Cambridge, Cambridge, UK.
RL Threlle (1966); J. Gen. Microbiol. 98: 1-11.
DR INTERPRO: IPR000185; -18-11-.
DR Pfam: PF01043; SecA_protectin; 1.
DR PRINTS: RRC0006; SECCA.
PT NON_TER.
P7 266 266
SQ SEQUENCE 266 AA: 30186 MW: A6F1AFBFBF5317E CRO64;

Query Match 1 0% Score 7; Db 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 1+e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY 355 SRRLODQ 401
Db 237 SRRLODQ 233

RESULT 45
ID 082397 PRELIMINARY: PRT: 284 AA.
AC 082397: 598 (TRENDEL) 08 (Genbank)
DT 01-NOV-1998 (TRENDEL) 08 Last sequence update)
DT 01-JUN-2000 (TRENDEL) 14 Last annotation update)
DN HYPOHECTICHL 32.6 KDa PROTEIN.
DS TIO2D 2.
OR "Cambridge" thillana (Youngster grass).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
ON [1]
RN "Cambridge".
AP SEQUENCE FROM N.A.
RA STRAIN-V. COLUMBIANA.
RN Rounsfey S.D., Lin X., Kaul S., Shea T.P., Pujiil C.Y., Mason T.M.,

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un-08-403-403-7, copy-45, 350,019,1994
Nov 9 11:14:16 2001

BA Shen M., Komling C.M., Fraser C.M., Chazotte J.L., Chazotte J.L., Venter J.C.
RL PubMed (Oct-1998) to the EMBL/GenBank/DBJ genomic sequence.
DR EMBL: AC005617; AAC63587.1
DR INTERPRO: IPR001092.
DR PFM: PF00010; Ref: 12624 NM: 22902850733AA4 CDS64.
SQ SQUONCE 264 AM:

Query Match 1.0% Score 7, DB 10, Length 264,
Best Local Similarity 100.0%, Tred 100, 4670, 0,
Matches 7, Conserved 0, Mismatches 0, Gaps
Oy 545 NWLVP 551
1111111
Db 255 NWLVP 261

RESULT 46
O22385
ID J02385
AA A 22385
DT 01-NOV-1996 (Transcribed: 01, Created)
DT 01-NOV-1996 (Translated: 01, Last sequence update)
DT 01-MAY-2000 (Transcribed: 13, Last annotation update)
CR 71145.5 PROTEIN.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoa; Chordata; Rhabditida; Rhabditidae.
OC Rhabditidae; Polidetae; Caenorhabditis.
RN 111111..._taxid=6335.
RP SEQUENCE PROK N.A.
RA Komurthy A.
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE PROK N.A.
EX MEDLINE=94150716; PubMed=7903398;
BA Milner R., Ainscough B., Anderson K., Baynes C., Berks M., Coulson A.,
BA Bontfield J., Burton J., Connell M., Cooper S., Cooper S., Coulson A.,
BA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
BA Jones M., Keshav J., Kirsten T., Lister N., Lettelle P.,
BA Lightning J., Lloyd C., Milner A., Mortimore B., O'Callaghan M.,
BA Paterson J., Peery C., Ritten L., Rooper S., Russell S., Shownkeen R.,
BA Thierry-Mieg D., Thomas K., Vaudin M., Vaughan K., Waterston R.,
BA Watson A., Weissbrock L., Wilkinson-Sproat J., Wohlman J.,
RF 2 Mb of continuous nucleotide sequence from chromosome III of C.
elegrans.
RL Nature 368 33-39(1994).
```

Query Match 1.0% Score 7, DB 10, Length 284,
Best Local Similarity 100.0%, Pred. No. 1,4e+02
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

Oy 545 N51UVP 551
Db 255 N51UVP 261

length 46
ID Q2385 PRELIMINARY: PRT: 288 AA.
CD 02385 AC Q2385.196 (TRIMMED). 01, (start sequence update)
DT 01-NOV-1996 CD 02385.196 (TRIMMED). 01, (start sequence update)
DD 01-MAY-2000 (TRIMMED). 13, (last annotation update)
DE T1A5.5 PROTEIN.
GN T1A5.5
LN 1145
OC Rhadilloidea: Metacoela: Nematozoa: Chromadorae: Rhadilloidea: Rhadillidae:
CC Rhadillidae: Polidoriinae: Ctenorhadtia.
OX NCBI_TaxID=6230;
RN NM_011496 PRONK N.A.
RA Memmery A.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DDJ databases.

SN SCIENCE PORN N.A.
RX MEDLINE=9450718; PubMed=7969398;
RA Wilson R., Anisescu F., Anderson K., Baynes C., Betts M.,
RA Bonfield J., Burton J., Connell H., Copsey T., Cooper V., Coulson A.,
RA Craxton M., Deas S., Du Z., Durbin R., Edwards J., El Molla Johnston L.,
RA Jones M., Keshav J., Kirsten J., Laister N., Lettelleir P.,
RA Lightning J., Lloyd C., Memmery A., Mortimore B., O'Callaghan M.,
RA Paterson J., Percy C., Rifkin L., Roopar A., Saunders D., Shomchen R.,
RA Thomson M.G., Thompson S., Vanham-Vanduijn M., Vaughan K.,
RA Watson A.C., Whitestock T.L., Wilkinson-Spratt J., Wohlman P.;
FT * 2 Mb of contiguous nucleotide sequence from chromosome III of C.
elephas 36833-39(1994).

[illegible][illegible][illegible]

OC	Eukaryotes; Fungi; Ascomycota; Schizosaccharomycetales;
OC	Schizosaccharomycetaceae; Schizosaccharomyces.
CC	SEQUENCE FROM N.A.
CC	STRAIN=J771.
CC	Kim S., Kim H., Kim M.J., Jin Y.H., Park S.D.;
CC	Submitted (May-1996) to the EMBL/GenBank/DDBJ databases.
CC	SEQUENCE FROM N.A.
CC	STRAIN=972.
CC	Volksteyn G., Wood V., Rajandream M.A., Barrell B.G.,
CC	Submitted (Sep-97) to the EMBL/GenBank/DDBJ databases.
CC	- - - INITIALLY BELONGS TO THE BOL4 / YBPA FAMILY. - - -
CC	This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed, usage by and for commercial entities requires prior agreement (see http://www.isb.ac.uk/announcements.html).
CC	EMBL: Z73498; CAN56579.1; ..
DR	EMBL: U51948; CAN06634.1; ..
DR	EMBL: X59438; CAN56579.1; ..
DR	INTERIM:P0102314; ..
DR	PIR: P01022; BOIA; 1.
QO	SEQUENCE 102 AA; 11806 MW; 1B35D7F2098EBD4 CRC64:
	Query Match Beat Local Statistally 100.0% Pred No. 14:
	Matches 7; Conservative 0; Mismatches 0;
OY	459 SPSSCH 465
OB	60 SPSSCH 66
RESULT 6	
RULE_BEST	STANDARD; PRT; 120 AA.
RULE_ALIGN	
AC	P09915;
D7	01-MAR-1989 (rel. 10; Created)
D7	01-MAR-1989 (rel. 10; Last sequence update)
D7	01-MAR-1989 (rel. 10; Last annotation update)
DE	505 RIBOSOMAL PROTEIN L18
DE	RPLA.
OC	Bacilli; Starothermophilus.
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;

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OC Bacillus/Saphylococcus group; Bacillus.
NR SIMILANCE FROM N.A.
EX MEDLINE+1093287; Pubmed=1985659;
RA Rasmikhishan V., Gerschman S.B.;
RT "Cloning, sequencing, and overexpression of genes for ribosomal
EL P. Biol. Chem. 266:980-985(1991)."
NR [2]
BP SEQUENCE: 67105935; Pubmed=3542552;
RA Khamayri F., Kumar M.
RP "The complete amino acid sequences of the 5 S rRNA binding proteins
RF 1S and L18 from the moderate thermophile Bacillus stearothermophilus
CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC
-- FUNCTION: THIS IS ONE OF THE 5 S RNA INTO THE LAMB PROTEIN.
CC -- SIMILANCE: BELONGS TO THE LAMB FAMILY OF RIBOSOMAL PROTEINS.
CC -- SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on
CC the use of this information on condition that acknowledgment is given to
CC modified and that this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/about/
CC or send an email to license@ebi.ac.uk).
CC CC EMU: M57624, AAA2702.1; ALT_SRO.
DB PTR_829102; RS5887.
DM INTERNO: IPRO01149;
DM PRNA: PRO0661; Ribosomal_L18P_1.
SO SEQUENCE: 120 AA; 13471 MW; 15974214289657 CRC64.

Query Match      1.0%. Score 7. DB 1. Length 120.
Local Similarity 100.0%. Pred No. 16.
Matches          0. Mismatches
                  0. Indels
                  0. Gaps

DB 61. REFQOLDS 63
OY 57 REFQOLDS 63

QUERY:
UNRE_LACFE
ID UNRE_LACFP STANDARD: PRT. 124 AA.
NC P62610.
DT 01 NOV-1992 (REL 23, Last sequence update)

```

OC Bacillus/Staphylococcus group; bacillus.
RA SOURCE FROM N.A.
RM SOURCE FROM N.A.
RX MEDLINE#0109287; PubMed#1985969;
BA Raaijmakers W., Gerichman S.E.;
BT "Cloning, sequencing, and functional expression of genes for ribosomal
RL protein L18 from the moderate thermophile Bacillus stearothermophilus".
RT J. Biol. Chem. 266:880-885(1991).
RM [2]
RP SEQUENCE #87105936; PubMed#354262;
RA Kikuchi T., Kikuchi M.;
BT "The complete amino acid sequence of the 5 S rRNA binding proteins
RT L5 and L18 from the moderate thermophile Bacillus stearothermophilus
RC ribosome". 210:85-90(1987).
CC - PUNCTION. THIS IS ONE OF 3 PROTEINS THAT MEDIATE THE ATTACHMENT OF
CC THE 5S RNA INTO THE LARGE RIBOSOMAL SUBUNIT.
CC - SIMILARITY: BELONGS TO THE LIPO FAMILY OF RIBOSOMAL PROTEINS.
CC CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL database,
CC the European Bioinformatics Institute. There are no restrictions on
CC modified and this statement is not removed. Users may add for comments
CC entries requires a license agreement (see http://www.ebi.ac.uk/annotation
CC or send an email to license@ebi.ac.uk).
CC CPM: M5753; AA02702.1; ALT.SQ.
DR INTERPRO: IPRO01149;
DR PRN: PRODBE1; Ribosome_L18bp_1.
SO Sequence 120 AA; 13471 MW; 1E5B74212883667 CNG64;

GARY MATCH 1.0% Score 7; DB 1 Length 120
Pct Local Similarity 100.0%; Pred No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

CY 57 REFSIDS 63
DB 63 Refids 67

RESULT 7
UNREF_LACIE
ID UNREF_LACIE STANDARD: PRT 124 AA.
AC P26310-1992 (Ref. 2) Created:
DT 01 NOV-1992 (Ref. 1) Last sequence update)

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DT 01-NOV-1995 (Rel. 32, Last annotation update)
DR ACID UREASE BETA SUBUNIT (BC 3.5.1.5) (DREA AMIDOHYDROLASE) .
NC UNREF.
CC Bacillus, Bacillus fermentum
CC Bacillus, Bacillus
CC Bacillus, Firmicutes
CC Lactobacillales
CC Lactobacillia
CC NC
NR SOURCE FROM N.A.
DR STRAIN:CM 5669.
PA Suzuki K., Takahashi M., Imanura S., Ishiava T.:
RL Submitted (JXX 1993) to the EMBL/Genbank/DBJ databases.
CC - SUBMITTER: JIMMY H. BERNARDINI (3) (BY SIMILARITY)
CC - SIMILARITY: NO OTHER UREASES BETA SUBUNTS.
CC
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CC
DR EMBL: D10605; BAA01459.1.
DR FSI: F01589.1; J0602019.
DR PRNA: P00659; Urease_beta.1.
NR Hydrolyase.
SQ SEQUENCE 124 AA: 14142 MW: 27139.6142005095 CRC64.

Query Match 1.0% Score 7; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches
Oy 280 KRYING 286
DB 12 KRYING 18
|||||||

RESULT 8
ID: HRA_ELEL
AC: P14550. STANDARD: PRT: 142 AA.
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1994 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 23, Last annotation update)
OS ELECTROBLIN ALPHA CHAIN
CS Electrophorus electricus (Electric eel)
CS Bakaryaya Metacos; Chondria Cretacea;
OC Actinopterygii; Mopterygii; Teleostei; Euteleostei; Osteichthys;

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OC Ooculiformes; Electrophoridae; Electrophorus.
NM (1)
RX MEDLINE=689228561; PubMed/713104;
PA Huber F., Bissulatti G.;
RT The primary structure of the hemoglobin of the electric eel
RU (1989) 10:1-10.
RU Biol. Chem. Hoppe-Seyler 370:245-250(1989).
DR PIR: S03399; S03399.
DR HSRP: P02018; 1000.
DR INTERPRO: IPR002318; -.
DR PFAM: PF00042; Globin; 1.
DR PRINTS: PR00613; ALPHABAM.
DR PROSITE: PS00027; Hemoglobin.
KW Hemoglobin (heme) ; Respiratory protein; Erythrocyte;
KW Acetylation.
FT MOD_RES 1 1 ACETYLATION (SITE 1 LEU64)
FT METAL 5 5 IRON (HEME PROXIMAL COORD.)
FT METAL 88 88 IRON (HEME PROXIMAL COORD.)
FO 50 SEQUENCE 142 AA; 15344 MW; 1A139E77ABF734 CMC64.

Query March 1 0% Score 7; DB 1
Best local Similarity 100.0% Pred. No. 19
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

CY 238 CIRENO 244
DB 66 CIRENO 72

RESULT 9
TATB-TATBN STANDARD: PRT: 186 AA.
AC 05/04/78; RA4359; 32 (Created)
AC MEDLINE=9350630; PubMed/7542800;
D7 01-OCT-2000 (Ref. 40; Last annotation update)
D8 SEC-DEPENDENT PROTEIN TRANSLOCASE PROTEIN TATB.
DE 01-OCT-2000 (Ref. 40; Last annotation update)
DE SEC-DEPENDENT PROTEIN TRANSLOCASE PROTEIN TATB.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
OC Haemophilus.
NM (1)
RX MEDLINE=9350630; PubMed/7542800;
PA Kleieman N.D., Bull C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,
PA McNamey K., Sutton G., Fittengh W., Fields C.A., Cooney J.D.,

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[illegible]

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CC DBML U3756; AAC9246.1;
CC DR EMBL: Z72200; CAA9758.1;
CC DR YPBL: Z687;
CC DR SGD: S0004038; RP808;
CC DR RHEMBOPO138; RPB080AL.82.1;
CC DR PRINTS: PR001395; RI8080AL.52.1;
CC DR PROSITE: PS00962; RI8080AL.52.1;
CC DR PROSITE: PS00963; RI8080AL.52.1;
CC DR PIR: p00962; DMO Binding Site SIMILARITY: Multisense family.
CC INTACT: 1; ACETYLATION (BY SIMILARITY);
CC FT MOD_RES 1 1
CC SEQUENCE 251 AA: 27831 MW: 2087DBE90A5FEBA8 CRC64;
CC

Query Match 1.0%; Score 7; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 388 TMAERN 354
Db 239 TMAERN 245
IIIIIII

RESULT_14
ID RS3A.SCHHO STANDARD: PROT: 251 AA.
D1 RS3A.SCHHO
D2 01-NOV-1995 (Rel. 32, Created)
D7 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 408 RI8080AL.PROTIN S1NC-N (91-A).
OE 01-NOV-1995 (Rel. 32, Last sequence update)
OS Schizosaccharomyces pombe (Fission yeast).
OC Schizosaccharomycetes; Ascomycota; Schizosaccharomycetales;
OC Baktiyoti; Fungi; Ascomycota; Schizosaccharomycetales;
NC Schizosaccharomycetes; Schizosaccharomycetes
NA 1
NP SEQUENCE FROM N.A.
RP STRAIN=972;
RA Orell C., Bowman S., Barrell B.C., Rajadheem M.A., Watan S.V.;
CC SCHIZOGENOMES: THERE ARE TWO GENES FOR S1 IN S.POME.
CC -1- SIMILARITY: BELONGS TO THE S3AE FAMILY OF RI8080AL PROTEINS.
CC -----
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Query Match      1.00: Score 7; DB 1; Length 251;
Beat Local Similarity 100.0%; Pval 0.0; Mismatches
OC 388 TEMKEN 394      0; Indels 0; Gaps 0;
OC 1111111111
DB 239 TITMANN 245
RESULT 13
RS08_YEAST
RS08_YEAST STANDARD: PRT: 251 AA.
AC P46654.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DR 405 RIBOSOMAL PROTEIN S0A (BACTERIAL ACID-BINDING PROTEIN S0A)
DR 405 RIBOSOMAL PROTEIN S0A (BACTERIAL ACID-BINDING PROTEIN S0A)
CN RS08 OR NM18 OR NM48 OR Y572 OR Y1604-8 OR L2118.
OC Saccharomyces cerevisiae (Baker's yeast)
OC Eukaryota: Fungi: Ascomycota: Saccharomycetes: Saccharomycetaceae:
OC Saccharomycetaceae: Saccharomycetaceae.
RN [1]
RP SEQUENCE FROM N.A.
RA Demariou M.A., Formosa T.G., Ellis S.R.:
RA Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
RP
RP SEQUENCE FROM N.A.
RA Andre B., Dreesen L.A.:
RA Submitted (Jan-1996) to the EMBL/GenBank/DBJ databases.
RP
RP SEQUENCE OF 92-55: 101-110 AND 134-145.
RA STRAIN=ATCC 14827 / SHQ2N.
RA MEDLINE=9190279; PUBMED=9018161;
RA Morwerk J., Blumengard A.:
RA Several amino acid sequence changes associated with growth of
RA Saccharomyces cerevisiae in 1.4 M NaCl. Evidence for osmotic
RA induction of glycerol dissimilation via the dihydroxyacetone
RA pathway. Ann. 372:5544-5554(1997).
CC 1.
CC PUNCTION: RIBS08.DNA SUBMITTED FOR THE ASSEMBLY AND/OR STABILITY OF
CC THE 405 RIBOSOMAL SUBUNIT.
CC
CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR S0 IN YEAST
CC
CC -1- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
CC
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CC      THAT HAVE CEASED PROLIFERATION BUT HAVE NOT YET BEGUN TO MIGRATE
CC      INTO THE OUTER LAYERS. IN RETINA, NEURON IS ALSO TRANSIENTLY
CC      DERESSED IN CELLS AS THEY WITHDRAW FROM THE MITOTIC CYCLE, BUT
CC      IT IS NOT KNOWN IF THIS OCCURS IN ALL TISSUES. FULL
CC      DIFFERENTIATION IN THE PERIPHERAL NERVOUS SYSTEM, ITS EXPRESSION
CC      CLOSELY FOLLOWS CELL PROLIFERATION
CC      -1- SIMILARITY BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC      TRANSCRIPTION FACTORS. ANOMAL SUBFAMILY
CC      -----
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      office which requires a license agreement (See http://www.ebi.ac.uk/ncn/news)
CC      or send an email to license@ebi.ac.uk.
DR      EMBL: G05977.CA10768.1..
DR      INTERPRO: IPR0010921..
DR      PIRAM: SPPO010; HLH: 1.
DR      Pfam: PF00008; HELIX_LOOP_HELIX_1
DR      SMART: SMO0008; HELIX_LOOP_HELIX_1
DR      ProDom: PD00008; HELIX_LOOP_HELIX_1
FM      Neurogenesis: Developmental protein; cell differentiation; Activator;
FM      Neurogenesis: Developmental protein; cell differentiation.
PT      DOVAIN 49 61
PT      DOVAIN 55 62
PT      DOVAIN 55 62
PT      DOVAIN 73 75
PT      DOVAIN 78 78
PT      DML_BIND 88 99
PT      DOVAIN 100 140
PT      DOVAIN 162 180
PT      DOVAIN 310 AA; 36707 MW; 56492PDA(CD)M1 CIRC44.
Query Match 1.0%; Score 7; DB 1; Length 330;
Matches 7; Consecutive 0; Hamming 0; Indels 0; Gaps 0;
Db 29 DELTAEN 35
```

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Page 40

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1. Qnry Match          1.0nry: Score 7; DB 1; Length 375;
Query Local Similarity 100.0n; Pctd 70.45;
Matrices 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Qy 454 TRNSPRT 460
Db 204 TRNSPRT 290

RESULT 17
AC AC007609; G53891; STANDARD; PRI; 407 AA.
AC AC007609; G53891;
DT 01-FEB-1995 (Rel. 3); (Created)
DT 30-MAY-2000 (Rel. 38; Last sequence update)
DT 30-MAY-2000 (Rel. 38; Last annotation update)
DE MEMBRANE PROTEIN MOSC.
GN MOSC.
OS Reticobium melioli (Simonrhizobium melioli).
OC Reticobiales, Proteobacteria, Alpha subdivision, Rhizobiaceae group;
OC Rhizobiaceae, Simionrhizobium.
RN 11)
RP SEQUENCE FROM N.A.
RA MENZIES J.S. 1976; PubMed8434659.
RA Murphy P.J., Tremn S.P., Gramsli M., de Bruijn P.J., Schell J.
RT "The Reticobium melioli rhizopine mos locus is a mosaic structure
RT facilitating its symbiotic regulation."
RT J. Bacteriol. 175:5193-5204(1993).
RN 12)
RP SEQUENCE FROM N.A.
RA STRAIN=BM220-3;
RA Bae J.Y. 1994; PubMed74551036.
RA Bae J.Y. 1994;
RT "Reticobium melioli lacking moa synthesizes the rhizopine seyllo-
RT inosamine in place of 3-O-methyl-seyllo-inosamine."
RT Microbiol. 141:1663-1690(1995).
CC 1) TRANSPORT A PRECURSOR FOR RHIZOPINE BIOSYNTHESIS AND BACTERIODIOS
CC OR THE FINISHED PRODUCT FROM THE BACTERIODIOS.
CC 2) SUBCELLULAR LOCATION: INTERAL MEMBRANE PROTEIN (PROBABLY).
CC 3) MAY BE PRODUCED BY THE USE OF IN-PROF ALTERNATIVE INITIATION
CC CODONS.
CC 4) THIS STRIS SPECIFICITY: EXPRESSED IN NODULES.
CC 5) THIS STRIS-PROT acity is co-ordinately regulated using collaboration
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CC AminoAcid; Metazoa; Chordata; Gnathata; Vertebrata; Euteleostomi;  
CC Anchoanidae; Aveae; Megachthae; Galiliformes; Phasianinae;  
RM [?];  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96145206; Pubmed-2537491;  
RZ "Identification key D.B., Lamont T., Estken R.L.;  
RL Proc. Natl. Acad. Sci. U.S.A. 86:1176-1182(1989).  
SC Pncr. MALL. Acid. Scl. u.s.a  
CC - FUNCTION: PROBABLE SECRETED REGULATORY PROTEIN.  
CC - LOCATION: BE SPEC TO THE INSULIN-LIKE GROWTH FACTOR BINDING  
CC - PROTIEN FAMILY: CBF-10/CIRP6/CIRP-/ISF-12/MOV PROTIEN SUPPLMILT.  
CC - SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE DOMAIN (CTCK).  
CC CC  
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DR EMBL_J04466; JAAI8661.J;  
DR PIR_A1428; AI448.I;  
DR INTERPRO: IPROO0159;  
DR INTERPRO: IPR008871;  
DR INTERPRO: IPR01007;-  
DR PFAM: Pf00007; Cyg_knotc_1.  
DR Pfam: Pf00145; IGFBP_1.  
DR Pfam: Pf00093; wvs_1.  
DR PROSITE: PS00222; IGF_BINDING; 1.  
DR PROSITE: PS01185; CTCK_1; 1.  
DR PROSITE: PS01208; WRCF; 1.  
DM Growth factor binding; Signal.  
FT SIGNAL 1 322  
FT CHAIN 1 322  
FT DOMAIN 98 164 WRCF  
FT DISUPTD 281 315 BY SIMILARITY  
FT DISUPTD 281 315 BY SIMILARITY  
FT DISUPTD 309 348 BY SIMILARITY  
FT DISUPTD 312 350 BY SIMILARITY  
FT DISUPTD 313 354 BY SIMILARITY  
SQ RESIDENCE 373 NAJ 40651 NM: 9576B53DE15DAE CRC64;
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CC	entiles requires a license agreement (see http://www.lab-abb.ch/announcements/) or send an email to license@lab-abb.ch .
DR	BML: L17071: AAA6301.1
DR	BML: U21753: AAA3134.1
KM	Transmembrane; Transport
FT	CHAIN 1 407
FT	CHAIN
FT	CHAIN 20 407
FT	INIT.MET 20 20
FT	TRANSMEM 63 85
FT	TRANSMEM 109 129
FT	TRANSMEM 157 177
FT	TRANSMEM 196 206
FT	TRANSMEM 225 275
FT	TRANSMEM 290 310
FT	TRANSMEM 316 316
FT	TRANSMEM 377 397
FT	VARIANT 64 64
FT	VARIANT 71 71
FT	VARIANT 100 100
FT	VARIANT 144 144
FT	VARIANT 174 214
FT	VARIANT 184 184
FT	VARIANT 219 219
FT	VARIANT 234 234
FT	COMPLCT 359 354
SD	SEQUENCE 407 AA: 4315 NM: 095046550AC7624F C9664; REF. 1: 1
Query Match	1.0%; Score 7; DB 1; Length 407;
Match	Local Similarity; ID 00; Pred. No. 43;
Matches	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	239 TAAWVG 245
DB	370 TAAWVG 376
RESULT 18	1111111
PROTEIN	STANDARD; PRT: 411 AA.
ID	TRE ANOP
AC	028669;
DT	15-JUL-1998 (Ref. 36, Created)

DT	01-NOV-1997 (rel. 35; Created)
DT	01-NOV-1997 (rel. 35; Last sequence update)
DT	15-JUL-1998 (rel. 36; Last annotation update)
DR	NITROBACTERIUM THERMOAUTOTROPICUM DSM 21331
DR	(NITROGENASE COMPONENT 1) (DINITROGENASE).
GC	Nitro.
GC	Methanobacterium thermoautotrophicum (strain Matburg / DSM 2133).
GC	Methanobacterium thermophilum, Methanobacteriales, Methanobacteriaceae.
CC	Methanobacterium.
CC	Sequence from N.A.
RP	Submitted (Feb-1997) to the EMBL/GenBank/DDJB databases.
RP	SEQUENCE FROM N.A.
RP	(1)
RP	(2)
RP	SEQUENCE OF 1,220 PPM N.A. 5975452.
RP	Hochstetler A., Schmitz R.A., Thauer R.K., Hedderich R.:
RT	The tungsten formylmethanofuran dehydrogenase from Methanobacterium
RT	thermoautotrophicum contains a sequence motif characteristic for
BA	Rut J., Bloemendal L.J., van der Vliet A., Thauer R.K., Hedderich R.,
CC	Bur J., Bloemendal L.J., van der Vliet A., Thauer R.K., Hedderich R.,
CC	-1- FUNCTION: THE KEY ENZYMATIC REACTIONS IN NITROGEN FIXATION ARE
CC	CATALYZED BY THE HETEROGENEOUS COMPLEX, WHICH HAS 2 COMPONENTS: THE
CC	-1- CATALYTIC ACTIVITY: 8 REDUCED FERREDOXIN + 8 H(+) + 2 O ₂ = 8
CC	Oxidized Ferredoxin + 2 NH ₃ + 16 ADP + 16 ORTHOPHOSPHATE.
CC	-1- SUBUNIT: Tetramer of two alpha and two beta chains that binds
CC	-1- SIMILARITY: BELONGS TO THE NIFD/NIFR/NIFE/NIFN FAMILY.
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CC	EMBL X87971, CA661219.1;
CC	INTERPRO: IPR000318;
CC	INTERPRO: IPR000310;
CC	Pfam: PF00146; oxidored_nitro_1; PALSE_NCG
CC	ProSITE: PS00090; NITROGENASE_1; 1
CC	oxidoreductases: Nitrogen fixation: MoLybdenum; Iron-sulfur
CC	SEQUENCE 470 AA: 51055 MS: 90090c10ab086dcd GR664.

Query Match 1.00; Score 7; DB 1; Length 470
Best Local Similarity 100.00; Pred. No. 55;

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[illegible]

RN [5]
 RP X.MAL CRYSTALLINAPRIN (2,15,ANGSTROMS).
 RA R.M.H. S. 1966; 66:17.
 RA Ko T. P., Saito M. K., Munayev F. N., Di Salvo M. L., Wang C., Wu S. H.,
 RA Abraham D. J.:
 RT Structure of human erythrocyte catalase.*
 RT ACTIVATION OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
 RT SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
 CC PEROXIDE.
 CC -1- CATALYTIC ACTIVITY: 2 H₂O₂ (2) = O₂ (2) + 2 H₂O (2).
 CC -2- COFACTOR: HEMOIN.
 CC -3- SUBSTRATE: HYDROXYPEROXIDE AND H₂O₂.
 CC -4- DISEASE DEFICIENCY IN CAT CAUSES ACATALASIA.
 CC -5- SPECIALLIZED LOCATION: PEROXISOMAL.
 CC -6- SIMILANTITY: BELONGS TO THE CATALASE FAMILY.
 CC -7- SIMILANTITY: BELONGS TO THE CATALASE FAMILY.
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 DR EMBL: X04076; CA237717.1; -
 DR EMBL: X04076; AAB59522.1; -
 DR EMBL: X04085; CA237721.1; J01NEO
 DR EMBL: X04085; CA237721.1; J01NEO
 DR EMBL: X04087; CA237721.1; J01NEO
 DR EMBL: X04088; CA237721.1; J01NEO
 DR EMBL: X04089; CA237721.1; J01NEO
 DR EMBL: X04090; CA237721.1; J01NEO
 DR EMBL: X04091; CA237721.1; J01NEO
 DR EMBL: X04092; CA237721.1; J01NEO
 DR EMBL: X04093; CA237721.1; J01NEO
 DR EMBL: X04094; CA237721.1; J01NEO
 DR EMBL: X04095; CA237721.1; J01NEO
 DR EMBL: X04096; CA237721.1; J01NEO
 DR EMBL: L13609; AAL16551.1; -
 DR EMBL: A00501; CS9H16
 DR EMBL: A00502; CS9H16
 DR EMBL: A00503; CS9H16
 DR EMBL: A00504; CS9H16
 DR EMBL: A00505; CS9H16
 DR EMBL: A00506; CS9H16
 DR EMBL: A00507; CS9H16
 DR EMBL: A00508; CS9H16
 DR EMBL: A00509; CS9H16
 DR EMBL: A00510; CS9H16
 DR EMBL: A00511; CS9H16
 DR EMBL: A00512; CS9H16
 DR EMBL: A00513; CS9H16
 DR EMBL: A00514; CS9H16
 DR EMBL: A00515; CS9H16
 DR EMBL: A00516; CS9H16
 DR EMBL: A00517; CS9H16
 DR EMBL: A00518; CS9H16
 DR EMBL: A00519; CS9H16
 DR EMBL: A00520; CS9H16
 DR EMBL: A00521; CS9H16
 DR EMBL: A00522; CS9H16
 DR EMBL: A00523; CS9H16
 DR EMBL: A00524; CS9H16
 DR EMBL: A00525; CS9H16
 DR EMBL: A00526; CS9H16
 DR EMBL: A00527; CS9H16
 DR EMBL: A00528; CS9H16
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 DR EMBL: A00533; CS9H16
 DR EMBL: A00534; CS9H16
 DR EMBL: A00535; CS9H16
 DR EMBL: A00536; CS9H16
 DR EMBL: A00537; CS9H16
 DR EMBL: A00538; CS9H16
 DR EMBL: A00539; CS9H16
 DR EMBL: A00540; CS9H16
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 DR EMBL: A00550; CS9H16
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 DR EMBL: A00553; CS9H16
 DR EMBL: A00554; CS9H16
 DR EMBL: A00555; CS9H16
 DR EMBL: A00556; CS9H16
 DR EMBL: A00557; CS9H16
 DR EMBL: A00558; CS9H16
 DR EMBL: A00559; CS9H16
 DR EMBL: A00560; CS9H16
 DR EMBL: A00561; CS9H16
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 DR EMBL: A00563; CS9H16
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 DR EMBL: A00567; CS9H16
 DR EMBL: A00568; CS9H16
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 DR EMBL: A00573; CS9H16
 DR EMBL: A00574; CS9H16
 DR EMBL: A00575; CS9H16
 DR EMBL: A00576; CS9H16
 DR EMBL: A00577; CS9H16
 DR EMBL: A00578; CS9H16
 DR EMBL: A00579; CS9H16
 DR EMBL: A00580; CS9H16
 DR EMBL: A00581; CS9H16
 DR EMBL: A00582; CS9H16
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 DR EMBL: A00593; CS9H16
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 DR EMBL: A00639; CS9H16
 DR EMBL: A00640; CS9H16
 DR EMBL: A00641; CS9H16
 DR EMBL: A00642; CS9H16
 DR EMBL: A00643; CS9H16
 DR EMBL: A00644; CS9H16
 DR EMBL: A00645; CS9H16
 DR EMBL: A00646; CS9H16
 DR EMBL: A00647; CS9H16
 DR EMBL: A006

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DR PRINTS: PRO0067; CATALASE.
DN PROSITE: PS00437; CATALASE_1.
FM PROSITE: PS00438; CATALASE_2.
EM Oxidoreductases; Peroxidase. Heme; Hydrogen peroxidase;
FM Peroxidases; hMBP; 3D-structure.
CC INTEREST 0
CC FUNCTION 0
CC ACT_SITE 147 147
CC ACT_SITE 357 357
SQ SEQUENCE 526 AA; 59625 MW; 70A1J39D124F5FE CR6C64;
PROXIMAL HEME LIGAND.

Query Match 1.0%; Score 7; DB 1; Length 526;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Db 477 AKAFFKE 597
IIIIIII
477 AKAFFKE 483

RESULT 27
CH60_EBNGR PRT; 569 AA.
AD CH60_EBNGR
AI 0-SEP-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last annotation update)
DT 15-OCT-1999 (Rel. 38, Last annotation update)
DS BACULOVIRUS CH60, MITOCHONDRIAL PRECURSOR (ASP 60).
GN HBPOD.
OS Euglena gracilis.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglenae.
RN BACULOVIRUS FROM N.A.
RA STRAIN=M10BSML.
RC Yeanlita S.; Simpson L.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RP SOURCE FROM N.A.
RC STRAIN=XZ.
SL Steiger A.;
LA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
LN BACULOVIRUS FROM N.A.
LC MONOCYTELLULAR ASSEMBLY MAY PREVENT MISFOLDING AND
CC IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE
CC REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED
CC -I- SUBCELLULAR LOCALIZATION TO THE MITOCHONDRIAL MATRIX.
CC -I- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC	modified and this statement is not removed, usage by and for commercial
CC	or send an email to license@db-ebc.ch
CC	EMBL_049553; AB093571.1
CC	HSP; P06133; JGRL
DR	INTERPRO: IPR002423
DR	PROSITE: PS00238, PS00239, PS00240
DR	PRINTS: P000248, COMPARTMENTS
DR	PROSITE: PS00296; CHAPERONIN60
DR	CHARACTER: ATP-binding, Transl. peptide, Mitochondrion; Heat shock.
FT	CHAIN 1 559
FT	CHAIN 2 559
FT	CHAIN 3 559
FT	CHAIN 4 559
FT	CHAIN 5 559
FT	CHAIN 6 559
FT	CHAIN 7 559
FT	CHAIN 8 559
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FT	CHAIN 147 559</

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Page 55

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US-08-403-B03-2 COPY 45 750.011g.TMP

Page 56

	RA	Johnston M., Andrews S., Birnham R., Cooper J., Ding H., Du Z.,
	RA	Ravello A., Fulton L., Gattung S., Greco T., Kirtlen J., Kuscha E.,
	RA	Jonaschewski K., Mekking U., Miller L., Jier W., Johnson D.,
	RA	Johnson N., Khan M., Pausley A., Peluso D., Rifkin B., Riesen S.,
	RA	Miller N., Mann M., Pauley A., Peluso D., Rifkin B., Riesen S.,
	RA	Talbot A., Trevasse E., Vignati D., Wilcox L., Wohlfahrt P., Vaulin M.,
	RA	Wilson R., Waterman R.,
	CC	Submitted (JAN-1995) to the EMBL/GenBank/DBS databases.
	CC	EMBL accession no. X68570.
	CC	
	CC	This SWISS-Prot entry is copyright . It is produced through a collaboration
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	CC	
	CC	POLY-SER. AA049310.1
	DR	EMBL_011910.1; AF049310.1; F;
	DR	SGD; S0004345; DBUS
	FT	DOMAIN 84 95 POLY-SER.
	FT	CONFLECT 140 140 R -> W (IN REF. 1).
	FT	CONFLECT 145 245 V -> W (IN REF. 1).
	FT	CONFLECT 245 350 S -> N (IN REF. 1).
	FT	CONFLECT 350 350 S -> N (IN REF. 1).
	FT	CONFLECT 354 354 T -> W (IN REF. 1).
	FT	CONFLECT 422 422 MISSING (IN REF. 1).
	FT	CONFLECT 492 602 R -> L (IN REF. 1).
	SO	SEQUENCE 603 AA: 65208 MW: 83594 ISCAI76EC4 CRC64;
QY	Query Match	Best Local Similarity 1.0%; Score 7; DB 1; Length 603;
	Matches 7; Consecutive 0; Mismatches 0; Indels 0; Gaps 0;	
YR	244 CDSPTP 250 369 CDSPTP 375	

GN BGLP ON 117C;
OC Bacillus subtilis;
OC Bacteria/Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
[1]
RN SOURCE FROM N.A.
RN STRAIN=168 / MARBURG.
BA MEDLINE=95169770; PubMed=7683710;
BA Le Cog D.G., Lindner C., Kneeger O., Steimetz M., Snelve J.;
BA New beta-glucosidase (bgl) genes in Bacillus subtilis: the bglp gene
BA of Bglp has both transport and regulatory functions similar to those
RT J. Bacteriol. 177:1537-1551(1995).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / MARBURG.
RC MEDLINE=95169770; PubMed=7683710;
RA Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
RA "Cloning and sequencing of a 39 kb region of the Bacillus subtilis
RA genome containing the hut and wpa loci.";
RL Microbiology 141:337-343(1995).
RL [3]
RP SEQUENCE OF 1-162 FROM N.A.
RC STRAIN=168;
RX MEDLINE=96304537; PubMed=8628237;
RX Beloin C., Hirschbuhl J., Le Begat F.;
RX The bglp gene product of a delta hut strain of
RT Bacillus subtilis acts as a beta-glucosidase and as a
RT repressible coil by a beta-lactamase inhibitor binding
RL site".
RL Mol. Gen. Genet. 250:761-766(1996).
-1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRYPHATE-DEPENDENT
CC PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR COORDINATE ACTIVE
CC TRANSDUCER OF PHOSPHATE AND CARBON METABOLISM IN BACTERIA
CC AND THE TRANSDUCING CHANNEL. THE IIA DOMAIN CONTAINS THE PRIMARY
CC PHOSPHOTRANSFER SITE (THE DONOR IS PHOSPHO-HRP); IIA TRANSFERS ITS
CC PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
CC THE SUBSTRATE.
CC -1- FUNCTION: PROTEIN N-PHOSPHOTRANSFERASE + SUGAR =
CC PROTEIN AESTILINE + SUGAR PHOSPHATE.

	RESULT	29
PRTN	BACST	STANDARD.
AD	PHOSPHANSEPHASE	PRT:
AC	P40739; Q45661;	609 AA.
DY	01-FEB-1995 (Feb. 31, Creted)	
DT	01-FEB-1995 (Feb. 31, Last sequence update)	
DE	01-FEB-1995 (Feb. 31, Last sequence update)	
DS	PROTEIN	
DR	PTS SYSTEM, BETA-D-GALACTOSIDASE-SPECIFIC INIAC COMPONENT (ETIAB-BG)	
DD	(BETA-D-GALACTOSE-PRIMER INIAC COMPONENT) (PHOSPHORANSEPHASE	
DE	INITIAL 1), AND COMPONENT) (DC 2..1..69) (Eti-BGL).	

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```

RT The coding sequences of 40 new genes (K1AA0041-K1AA0080) deduced by
RT analysis of cDNA clones from human cell line K562.
RT DNA Ref. 1,122,229(1994).
CC
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.emb-nb.ch/announcements/
CC or send an email to license@emb-nb.ch).
DR EMBL: D35548; BAA07551.1; -.
DR Hypothetical protein.
KW
KW SEQUENCE 1659 AA; 191108 MW; 57B11CC47BE3EDD CRC64;
Db
Oy 554 RDYAVYL 560
Db 740 RDYAVYL 746
| | | | |
RESULT 42
PROB YEAST
PR08 YEAST
STANDARD: PRT: 2413 AA.
AD P33341
DT 01-FEB-1994 (rel. 28; Created)
DT 01-FEB-1994 (rel. 28; Last sequence update)
DT 01-NOV-1995 (rel. 32; Last annotation update)
CM PDB OR RNA5 OR DB3 OR DNA33 OR VHA15C.
CM Saccharomyces cerevisiae (Baker's yeast).
CC Eukaryote; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
CC Saccharomycetaceae; Saccharomycos.
CC
CC SEQUENCE FROM N.A.
RP MEDLINE:95304817; PubMed:7785334;
RP Hodges P.E., Jackson S.P., Brown J.D., Beggs J.D.,
RP yeast 11:371-372(1995); conservation of the Pribic splicing factor *.
RL yeast 11:371-372(1995).
RN
RN SEQUENCE FROM N.A.
RP MEDLINE:7818707;
RP Shue J.E., Toyo U.H., Johnston L.H.;
RT The budding yeast us anp1 Pribic is a highly conserved protein which
RT links RNA splicing with cell cycle progression.
RT Nucleic Acids Res. 21:3555-3564(1994).

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Mon Apr 9 11:14:15 2001

us-08-403-803-2_copy_45_750.011g.tif

Page 75

FN	31	GENE FROM M. ABS72.
FE	32	STRAIN-528BC / AB972.
FC	33	MEDLINE=4476003; PubMed=601229;
FA	34	Johnson M., Andrews S., Brinham R., Cooper J., Ding H., Dover J.,
EA	35	De Z., Favallo A., Fulton D., Gidding S., Gillingham Y.,
DA	36	Latteille P., Louis E.J., Macci C., Mirdis E., Meneses S., Moutar L.,
CA	37	Nhan M., Rifkin L., Riles L., St Peter H., Tzevakis E., Vaughan K.,
BA	38	Vignati D., Wilcox L., Wohltman P., Waterston R., Wilson R.,
AT	39	Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT	40	viii.
RL	41	Science 265:2077-2082(1994).
RL	42	GENE ACTERIZATION.
RA	43	MEDLINE=8822580; PubMed=265658;
EA	44	Jackson S.P., Joshiy M., Begg J.D.;
CA	45	"Cloning of the RNA8 gene of Saccharomyces cerevisiae: detection of
CC	46	pre-mRNA splicing." demonstration that it is essential for nuclear
CC	47	mol. cell. Biol. 8:1057-1075(1988).
CC	48	FUNCTION OF INVOLVED IN PRE-MRNA SPLICING. US SNRNP PROTEIN
CC	49	IN CELL CYCLE BINDS RNA.
CC	50	SUBCELLULAR LOCATION: NUCLEAR.
CC	51	- SIMILARITY: STRONG. TO C. ELONGAS PROTEIN C503.6.
CC	52	This SNRP-proc. entry is copyright. It is produced through a collaboration
CC	53	between the Swiss Institute of Bioinformatics and the EMBL outstation
CC	54	the European Bioinformatics Institute. There are no restrictions on its
CC	55	use by non-profit institutions as long as its content is in the public
CC	56	domain and commercial entities require a license agreement (see http://www.embnet.org/licenses/
CC	57	or send an email to license@ebi.ac.uk).
CC	58	-----
DR	59	EMBL: J29421; AAC67044.1;
DR	60	EMBL: U00027; AAB58011.1; -;
DR	61	PIR: S34670; S34670.
DR	62	PIR: S34605; S34605.
DR	63	SWISS: S34670; S34670.
DR	64	SWISS: S34605; S34605.
FM	65	mRNA processing; mRNA splicing; Spliceosome; Nuclear protein;
FM	66	RNA-binding;
FM	67	DOMAIN
FT	68	20 5
FT	69	25 2
FT	70	50 56
FT	71	72 78
FT	72	DOMAIN
FT	73	388 420
FT	74	CONFLICT
FT	75	(18 REF. 2).

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Page 16

A:Status: preliminary
A:Molecule type: mRNA
A:Accession: T44854
A:Cross-references: EMBL:AL110760
A:Experimental source: clone DKFZ586B1621
C:Genetics:
A:Note: DKFZ586B1621.1

Query Match 1.1% Score 8; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 29 LITERMGS 268
DB 29 LITERMGS 36

RESULT 6

C72261 spermidine/putrescine ABC transporter, permease protein - *Thermotoga maritima* (strain MS88)
C:Species: *Thermotoga maritima*
C:Date: 11-Jun-1999 sequence_revision 11-Jun-1999 text_change 21-Jul-2000
C:Accession: C72261
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gilm, M.L.; Dodson, R.J.; Hall, D.H.; Hickey, E.K.; Peterson, J.D.; Nelson, M.C.; Currell, H.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Heidelberg, J.; Sutton, G.G.; Field, N.; Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of *Thermotoga maritima*.
A:Reference number: N7200; NCID:92487316
A:Molecule type: DNA
A:Status: preliminary
A:Cross-references: DB:AE01791; DB:AE00512; NCID:94981939; PDB:1A0D448.1; PID:94081939; TIGR:TM1378
A:Genes: TM1378
C:Superfamily: spermidine/putrescine transport system permease protein pol1

Query Match 1.1% Score 8; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 605 RLODPKMS 612
DB 150 RLODPKMS 157

RESULT 7

Query Match 1.1% Score 8; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 377 WMBEFCOL 384
DB 413 WMBEFCOL 420

RESULT 9

747503 ribonucleic protein PRK21.210 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (imported)
C:Date: 20-Apr-2000 sequence_revision 20-Apr-2000 text_change 20-Apr-2000
C:Accession: 747503
R:Jordan, N.; Banger, S.; Wiedemann, R.; Voss, H.; Unold, M.; Meves, H.W.; Lemcke, K.; Mayer, K.F.X.; Queller, F.; Salas, A.; Nature 399, 323-329, 1999
A:Reference number: E24667
A:Molecule type: DNA
A:Status: preliminary
A:Cross-references: DB:AL118657
A:Experimental source: CULTIVAR Columbia; BAC clone PRK21
C:Genetics:
A:Reference number: 3
A:Note: PRK21.210

Query Match 1.1% Score 8; DB 2; Length 989;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 236 RNCIMNAV 243
DB 545 RNCIMNAV 552

RESULT 10

A48773 ribonuclease P (BC 3.1.26.5) precursor, mitochondrial - yeast (*Saccharomyces cerevisiae*)
N:Alternative names: protein YNL091c
C:Species: *Saccharomyces cerevisiae*
C:Date: 19-May-1995 text_change 21-Jul-2000
C:Accession: A48773; S49639; S61340; S61339; S10802
R:Dang, Y.L.; Martin, N.C.; J. Biol. Chem. 268, 19791-19796, 1993
A:Title: Yeast mitochondrial RNase P: Sequence of the RNP2 gene and demonstration that its product is a protein subunit of A:Reference number: A48773; NCID:93314919

T44854 molybdenum-binding periplasmic protein [Imported] - *Arthrobacter nitrofunovans* plasmid pMO1
C:Species: *Arthrobacter nitrofunovans*
C:Date: 21-Jun-2000 sequence_revision 21-Jun-2000 text_change 18-Feb-2000
C:Accession: T44854
R:Brandt, R.
A:Title: The EMBL Data Library, February 1999
A:Reference number: 222860
A:Accession: T44854
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Cross-references: EMBL:Y10817; PDB:1AA7176.1
C:Genetics:
A:Gene: modA
A:Keywords: molybdenum-binding periplasmic protein

Query Match 1.1% Score 8; DB 2; Length 260;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 595 PRTNSNF 602
DB 53 PRTNSNF 60

RESULT 8

T30154 hypothetical protein R57.1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 sequence_revision 15-Oct-1999 text_change 18-Feb-2000
R:Revello, T.; Rifkin, L.; Chiappelli, B.
A:Title: The EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid R57.
A:Reference number: 220745
A:Accession: T30154
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-751 <FAV>
A:Cross-references: EMBL:U88179; PDB:1AB5260.1; GSPDB:GM00208; GSPB:R57.1
A:Genes: R57.1
A:Map position: X
A:Keywords: 40/1; 145/1; 230/1; 275/3; 313/1; 344/2; 405/1; 453/2; 576/2; 671/2; 713/3

A:Accession: A48773
A:Molecule type: DNA
A:Residues: 1-1302 <DNA>
A:Cross-references: EMBL:106309; NCID:9172441; PDB:1AA0158.1; PID:9172442
A:Note: parts of this sequence, including the amino end of the mature protein, were confirmed by peptide sequencing
R:Gentile, S.; Bowman, S.
A:Title: The EMBL Data Library, November 1994
A:Reference number: S49627
A:Accession: T44854
A:Molecule type: DNA
A:Residues: 1-1302 <GENB>
A:Cross-references: EMBL:246660; NCID:9575702; PID:9575712; MIPS:YML091c
R:Morales, M.C.; Dang, Y.L.; Lou, S.C.; Gilm, M.L.; Martin, N.C.
A:Title: A 105-kDa protein is required for yeast mitochondrial RNase P activity.
A:Reference number: S61339; NCID:9308566
A:Accession: S61340
A:Molecule type: DNA
A:Residues: 123-138 'X' 140-142 <NON>
A:Accession: S61339
A:Molecule type: protein
A:Keywords: hydroxylase; mitochondrial; RNA binding; RNA processing
A:Comment: The mitochondrial ribonuclease P holoenzyme includes a specific RNA chain.
C:Genetics:
A:Gene: SCD:RPM2
A:Cross-references: SCD:50004556; MIPS:YML091c
A:Reference number: 3
A:Note: PRK21.210

Query Match 1.1% Score 8; DB 2; Length 1202;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 673 SRVPSKA 680
DB 453 SRVPSKA 460

RESULT 11

T30858 glucosyltransferase - *Streptococcus salivarius*
C:Species: *Streptococcus salivarius*
C:Date: 22-Oct-1999 sequence_revision 22-Oct-1999 text_change 22-Oct-1999
C:Accession: T30858
R:Limpson, C.L.; Giffard, P.M.; Jacques, N.A.
A:Title: *Streptococcus salivarius* ATCC 25975 possesses at least two genes coding for primer-independent glucosyltransferase

A:Reference number: 220909; NID:9512137
 A:Accession: AF03985
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residue: 1-1577 <END>
 A:Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: functional analysis and comparative genomics
 A:Gene: gtfm

Query Match 1.0%; Score 8; DB 2; Length 1577;
 Best Local Similarity 100.0%; Pred No. 28;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1091 NID:DELTA 1098

RESULT 12
 C:Species: *Methanobacterium thermoautotrophicum* (strain Delta H)
 C:Date: 03-Dec-1999 sequence revision 03-Dec-1997 text change 13-Aug-1999
 C:Accession: C69220
 C:Residue: 1-1577 <END>
 C:Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: functional analysis and comparative genomics
 A:Reference number: A59000; NID:9607514
 A:Accession: C69220
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Residue: 1-1577 <END>
 A:Cross-references: GB:AE000795; GB:AE000656; NID:94521036; PID:AA84529.1; PID:94521056
 A:Experimental source: strain Delta H
 C:Gene: gtfm
 C:Superfamily: *Escherichia coli* ribosomal protein L29

Query Match 1.0%; Score 7; DB 2; Length 64;
 Best Local Similarity 100.0%; Pred No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 21 LID:AAE 27

OR 18 LID:AAE 24
 11111111
 DB 76 LID:AAE 82

RESULT 15
 C:Species: *Schizosaccharomyces pombe*
 C:Date: 03-Dec-1999 sequence revision 03-Dec-1999 text change 21-Jan-2000
 C:Accession: J13980
 C:Residue: 1-102 <END>
 C:Title: The complete amino acid sequence of the 5 S rRNA binding protein L5 and L16 from the moderate thermophile *Bacillus subtilis* strain 9724; consaid c1609
 A:Reference number: 221865
 A:Accession: J13980
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residue: 1-102 <END>
 A:Cross-references: EMBL:289759; PDB:GM16898.1; GSPDB:GM00067; SPOB:SPC1689.06c
 A:Gene: vll1; SPOB:SPC1689.06c
 A:Map position: 2
 C:Superfamily: beta protein

Query Match 1.0%; Score 7; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred No. 25;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 60 SPOB: 66

RESULT 16
 C:Species: *Bacillus stearothermophilus*
 C:Date: 30-Sep-1991 sequence revision 30-Sep-1991 text change 30-Jun-1993
 C:Accession: J39402; J39402
 C:Residue: 1-197 <END>
 C:Title: The complete amino acid sequence of the 5 S rRNA binding proteins L5 and L16 from the moderate thermophile *Bacillus subtilis* strain 9724; consaid c1609
 A:Reference number: A23102; NID:97105936
 A:Accession: J39402
 A:Status: preliminary
 A:Molecule type: protein
 A:Residue: 1-197 <END>
 A:Cross-references: EMBL:111111; PDB:1L1111; GSPDB:GM00079
 A:Gene: vll1; SPOB:SPC1689.06c
 A:Map position: 2
 C:Superfamily: beta protein

RESULT 13
 C:Species: *Deinococcus radiodurans* (strain R1)
 C:Date: 03-Dec-1999 sequence revision 03-Dec-1999 text change 11-Mar-2000
 C:Accession: F05233
 C:Residue: 1-1577 <END>
 C:Title: Complete genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A:Reference number: W7520; NID:20036996
 A:Accession: F05233
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residue: 1-1577 <END>
 A:Cross-references: GB:AE001910; GB:AE000513; NID:94518198; PID:AAE10098.1; PID:94518209; TIGR:DB0518; GSPDB:GM00077
 A:Experimental source: strain R1
 C:Gene: gtfm
 C:Superfamily: *Escherichia coli* ribosomal protein L29

Query Match 1.0%; Score 7; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 118 NID:AAE 124

RESULT 14
 C:Species: *Sulfolobus solfataricus* (strain 97-2)
 C:Date: 07-Sep-1990 sequence revision 07-Sep-1990 text change 08-Oct-1999
 C:Accession: S03214
 C:Residue: 1-1577 <END>
 C:Title: Complete genome sequence of the hyperthermophilic archaeon *Sulfolobus solfataricus* strain 97-2; consaid c1609
 A:Reference number: S03214
 A:Accession: S03214
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residue: 1-1577 <END>
 A:Cross-references: EMBL:X07234; NID:945703; PID:CA30213.1; PID:945707

Query Match 1.0%; Score 7; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A:Title: Cloning, sequencing, and overexpression of genes for ribosomal proteins from *Bacillus stearothermophilus*.
 A:Reference number: A39085; NID:91091287
 A:Accession: J13980
 A:Molecule type: DNA
 A:Residue: 9-111 <END>
 A:Cross-references: GB:M57624; NID:94521036; PID:AA84529.1; PID:94521056
 A:Experimental source: strain Delta H
 C:Gene: gtfm
 C:Superfamily: *Escherichia coli* ribosomal protein L29

Query Match 1.0%; Score 7; DB 2; Length 120;
 Best Local Similarity 100.0%; Pred No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 61 NID:AAE 67

RESULT 17
 C:Species: *Deinococcus radiodurans* (strain R1)
 C:Date: 03-Dec-1999 sequence revision 03-Dec-1999 text change 17-Mar-2000
 C:Accession: F05233
 C:Residue: 1-1577 <END>
 C:Title: Complete genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A:Reference number: W7520; NID:20036996
 A:Accession: F05233
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residue: 1-1577 <END>
 A:Cross-references: GB:AE001910; GB:AE000513; NID:94518198; PID:AAE10098.1; PID:94518209; TIGR:DB0518; GSPDB:GM00077
 A:Experimental source: strain R1
 C:Gene: gtfm
 C:Superfamily: *Escherichia coli* ribosomal protein L29

Query Match 1.0%; Score 7; DB 2; Length 133;
 Best Local Similarity 100.0%; Pred No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 694 PDB:AAE 700

OR 18 LID:AAE 24
 11111111
 DB 76 LID:AAE 82

P. Demianova, M.A.: Formosa, T.G.; Ellis, S.R.
submitted to the EMBL Data Library, August 1995
A:Accession: U08672
A:Accession: S59364
A:Molecule type: DNA
A:Reads: 1-257 <END>
A:Cross-references: EMBL:U08672; PDB:MAC9276.1; PDB:G1002792
Submitted to the EMBL Data Library, December 1995
A:Accession: S61618
A:Molecule type: cDNA
A:Reads: 1-255 <END>
B:Andrzej, B.; Dursztarski, L.A.
A:Cross-references: EMBL:X94607; NID:g1181264; PIDN:CA66295.1; PID:g1181269
A:Accession: S64876
A:Reference number: S64872
Sequence Database, May 1996
A:Molecule type: DNA
A:Reads: g1-253 <END>
A:Cross-references: EMBL:g1-273220; MIPS:TIR048v; NID:g1360382; PIDN:CAA97576.1; PID:g1370302
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SCP.NMB1B: YST7
A:Map position: 128
A:Map coordinates: SCD:S0004038; MIPS:TIR048v
A:Introns: 30/3
C:Superfamily: Yeast ribosomal protein S1.e
C:Keywords: protein biosynthesis; ribosome

Query Match 1.0%; Score 7; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 388 TERAEEN 394
 |||||
OB 240 TERAEEN 246

RESULT 31

G72296
C:Description: Ribosomal protein RPL079 - Thermotoga maritima (strain MS8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 Sequence Revision 11-Jun-1999 seq.cchange 21-Jul-2000
C:Accession: G72296
R:Macdon, K.E.; Layton, R.A.; Gill, S.R.; O'Leary, M.T.; DeLong, E.J.; Hickey, F.K.; Peterson, J.D.; Wilson, M.C.
R:Chen, M.H.; Stewart, A.M.; Colston, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Metcalberg, J.; Sutton, G.C.; Fietz,
C.M.
J:Accession: J03333-325, 1999
M>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.

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Oy: 442 EOPROKS 448
Db: 253 EOPROKS 259

RESULT: 33

A:Reference number: A7200; M01D:99487316
A:Accession: M01D99487316
A:Status: preliminary
A:Molecule type: DNA
A:Residue: 1-264 -ASNS-
A:Cross-reference: DB:AB001768; DB:AB000512; M1D:94981619; PIDN:AA036156.1; PID:94981624; TIGR:M1079
A:Genetic:
C:Genetic:
A:Genetic: TM1079

Query Match
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy: 516 ELYENKY 522
Db: 16 ELYENKY 22

RESULT: 32

hypoetical protein T11A.5 - Caenorhabditis elegans
T24824
C:Species: Caenorhabditis elegans
C:Species: C. elegans
C:Accession: T24824
R:McMurry, A.
submitted to the EMBL Data Library, May 1996
Accession: T24824
Accession: T24824
A:Status: preliminary; translated from DB/EMBL/DBJ
A:Molecule type: DNA
A:Cross-reference: M1D:94981619
A:Cross-reference: EMBL:272515; PIDN:CAA6685.1; GSPDB:GN00023; CESP:T11A.5
A:Experimental source: clone T11A5
C:Genetics:
A:Genetic: CESP:T11A.5
A:Genetic: CESP:T11A5
A:Intron: 202/2

Query Match
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Mon Apr 9 11:14:14 200

us-08-403-803-2_copy_45_750.011g.rp

Page 4

MON Apr 9 11:14:14 200

US-08-403-803-2_copy_45-750.0119.rp

Page 4

Hypothetical protein MO281.4 - *Ctenorhabdites elegans*
C|Species: Ctenorhabdites elegans
C|Date: 15-Oct-1999 sequence-revision 15-Oct-1999 steXl-change 15-Oct-1999
C|Accession: T13673
A|Accession: T13673
submitted to the EMBL Data Library, October 1996
A|Reference number: Z19780
A|Accession: T13673; translated from CB/EMBL/DDBJ
A|Accession: T13673; translated from CB/EMBL/DDBJ
A|Molecule type: DNA
A|Residues: 1-313 <EID>
A|C|Cross references: EMBL:Z81102; PDB:CBM03203.1; GSPDB:GN00023; CESP:MO281.4
A|Experimental source: clone MO281
A|Gene: CESP:MO281.4
A|Map position: 4
A|Introns: 31/2; 195/3; 228/1

Query Match
Match Local Similarity 1.0%; Score 7; DB 2; Length 313;
Matches 7; Conservative 0; Pred No 71;
Mismatch 0; Indels 0; Gaps 0;

OY 370 RTILFAS 376
|||||||
91 RTILFAS 97

RESULT 34
Enterococcus faecalis
Probable pheromone-responsive regulatory protein X - Enterococcus faecalis pCF10
C|Species: Enterococcus faecalis
C|Date: 30-Jun-1992 sequence-revision 30-Jun-1992 steXl-change 15-Oct-1999
C|Accession: U00006; translated from F00006
S|Accession: U00006; translated from F00006
J|Bacteriol. 172: 7650-7664, 1991
Article: Molecular and genetic analysis of a region of plasmid pCDF containing positive control genes and structural gene

```

OY      600 SKRSRL 606
        |||||||
DB      46 SKRSRL 54

RESULT 35
C:Spec: conserved hypothetical protein - Delnoccocus radiodurans (strain RI)
C:Access: Delnoccocus radiodurans
C:Release: 03-Dec-1999 ;sequence-revision 03-Dec-1999 ;text-change 17-Mar-2000
C:Gene: B1552 J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Haft, D.H.; G
M: Shon, M.O.; Venter, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaslavski, C.; Makova, K.S.;
S: Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 266, 1571-1577, 1999
P: 1999-09-09 The radioresistant bacterium Delnoccocus radiodurans RI.
A:Accession: AF5450; NCID 20036896
A:Accession: B75382
A:Status: Preliminary
A:Keywords:
A:Keywords: 1-118 <M>
A:Cross-reference: GB:AE001999; GB:AE000513; NID:96459316; PIDD:ANF11121; I: PTD:96459321; TIGR:DB156
A:Experimental source: strain RI
A:Gene: DB1560
A:Map position: 1

Query Match
Beit Local Similarity 1.0%; Score 7; DB 2; Length 318;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      471 L6GNDP 477
DB      105 L6GNDP 111

```

11. L. L. NELSON, JR., and D. J. NELSON, *J. Polym. Sci. Polym. Chem. Ed.*, **10**, 1131 (1972).

A:Status: preliminary
A:Molecular type: DNA
A:Accession: J137550.0
A:Cross-references: DB:M64970; NID:J150552; PDB:AAA6845.1; PID:J150553
C:Genetics:
A:Genome: Plasmid

Query Match 1.00; Score 7; DB 2; Length 317;
Best Local Similarity 100.00; Pred. No. 71;

HYPOPHOSPHITE DEHYDROGENASE-RELATED ENZYME
 Cytosolic hypophosphite dehydrogenase from *Escherichia coli*
 C.D. Cole, 15-Oct-1999 sequence, revision 15-Oct-1999 | text_change 04-Mar-2000
 C.Accession: Z75865
 R. Langston, C. M. Schmidt, P. J. Gillam, B.
 J. Langston, J. M. Langston, J. M. Langston, 1997
 A.Description: The sequence of C. elegans cosmid T0594.
 A.Reference number: Z20103
 A.Accession: Z75865
 A.Status: preliminary; translated from GD/MD1/DD02

hypothetical protein
C:Species: Caenorhabditis
C:Date: 15-Oct-1999
C:Accession: J25869
R:Langston, Z.; Mohr, J.
submitted to the EMBL
A:Description: The
A:Reference number:
A:Accession: J25869
A:Status: preliminary

on 15-Oct-1999 **text_change** 04-Mar-2000
 O. B.
 April 1997
 rgans cosmid T09B4.
 on GB/EMBL/DBJ

Best Local Similarity: 100.0%; Pred. No. 91;
Matches: 7; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
QY 380 ERFGLG 386
DB 200 ERFGLG 206

RESULT 49

rod shape protein - Chlamydia pneumoniae (strain CW029)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 sequence, revision 23-Apr-1999 #text_change 05-May-2000
C:Accession: C72026.11. M: Martine, R.; Lamm, C.; Fan, J.; Olinger, L.; Grimwood, J.; Davis, R.W.; Stephens, R.S.
Nucleic Acid: 21, 385,389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MIMD:92060606
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-415 <NR>
A:Cross-references: GB:AE001667; GB:AE001363; MIMD:94377171; PID:RAD19005.1; PID:94377184
C:Genetic: strain CWD029
A:Gene: rodA
C:Superfamily: rod shape-determining protein

Query Match 1.0%; Score 7; DB 2; Length 415;
Best Local Similarity: 100.0%; Pred. No. 92;
Matches: 7; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
QY 380 ERFGLG 386
DB 318 ERFGLG 324

RESULT 50

Integral membrane protein, MRAP family - Deinococcus radiodurans (strain RJ)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 sequence, revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: G73363
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.R.; Peterson, J.D.; Dodson, R.J.; Haft, D.H.; Gwin, M.L.; Nelson, M.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalevsky, C.; Makarova, K.S.; Aravind, L.; Daly, M.
Science 286:1571-1577, 1999.
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RJ.
A:Reference number: A75250; MIMD:2003896
A:Accession: G73363

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-415 <NR>
A:Cross-references: GB:AE000012; GB:AE000513; MIMD:9459473; PID:ARF1265.1; PID:9459478; TIGR:DR1709; GSPDR:GNC0077
A:Experimental source: strain RJ
C:Genetic: strain RJ
A:Gene: DR1709
A:Molecule type: DNA
C:Superfamily: natural resistance-associated macrophage protein 1

Query Match 1.0%; Score 7; DB 2; Length 436;
Best Local Similarity: 100.0%; Pred. No. 96;
Matches: 7; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
QY 484 LQINCR 490
DB 95 LQINCR 101

Search completed: April 6, 2001, 16:57:03
Job time: 151 sec

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDWARD R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FIP-001
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ. ID NO.: 18:
SOURCE: CHAUCHERES
SEQ. ID NO.: 18
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..707
OTHER INFORMATION: PSMA
PCT-US95-11720-18

Query Match 100.0% Score 706 DB 4 Length 707
Best Local Similarity 100.0% Pct. No. 0
Matches 706: Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 SSNKAITPRHNAKAFLEDAKAKETKFLPTQIPHLACITQDFQALAKIOSQKRG 60
2 SSNKAITPRHNAKAFLEDAKAKETKFLPTQIPHLACITQDFQALAKIOSQKRG 61
61 LQVEAHAYVLLSPKTHPTVTSINQKNEIFPISLPFPPGVEVSDIYPPSNAP 120
62 LQVEAHAYVLLSPKTHPTVTSINQKNEIFPISLPFPPGVEVSDIYPPSNAP 121
121 SPQGPBQDLVYVNAKTEPFLKEDKINCSQKLYVARGVQGNVNAQLAGAG 180
122 SPQGPBQDLVYVNAKTEPFLKEDKINCSQKLYVARGVQGNVNAQLAGAG 181
181 VILSDADYFAKCVASPPGKMLPGQGVQGNILMLNAGDPLPGYANETARGIA 240
182 VILSDADYFAKCVASPPGKMLPGQGVQGNILMLNAGDPLPGYANETARGIA 241
241 EAVGLPSIPVPIGTDQKLEKKGASAPPSNRKSLKVPYNGPGTNGSTORYM 300
242 EAVGLPSIPVPIGTDQKLEKKGASAPPSNRKSLKVPYNGPGTNGSTORYM 301
301 HINSHETRTIYVIGTIGKAVPEPVYVILGSHQSWTGTIDRQGAAYHETVSGCT 360
302 HINSHETRTIYVIGTIGKAVPEPVYVILGSHQSWTGTIDRQGAAYHETVSGCT 361

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDWARD R.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/41426
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ. ID NO.: 2:
SOURCE: CHAUCHERES
SEQ. ID NO.: 2
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US-95-553-2

Query Match 100.0% Score 706 DB 1 Length 750
Best Local Similarity 100.0% Pct. No. 0
Matches 706: Conservative 0 Mismatches 0 Indels 0 Gaps 0

1 SSNKAITPRHNAKAFLEDAKAKETKFLPTQIPHLACITQDFQALAKIOSQKRG 60
2 SSNKAITPRHNAKAFLEDAKAKETKFLPTQIPHLACITQDFQALAKIOSQKRG 61
61 LQVEAHAYVLLSPKTHPTVTSINQKNEIFPISLPFPPGVEVSDIYPPSNAP 120
62 LQVEAHAYVLLSPKTHPTVTSINQKNEIFPISLPFPPGVEVSDIYPPSNAP 121
121 SPQGPBQDLVYVNAKTEPFLKEDKINCSQKLYVARGVQGNVNAQLAGAG 180
122 SPQGPBQDLVYVNAKTEPFLKEDKINCSQKLYVARGVQGNVNAQLAGAG 181
181 VILSDADYFAKCVASPPGKMLPGQGVQGNILMLNAGDPLPGYANETARGIA 240
182 VILSDADYFAKCVASPPGKMLPGQGVQGNILMLNAGDPLPGYANETARGIA 241
241 EAVGLPSIPVPIGTDQKLEKKGASAPPSNRKSLKVPYNGPGTNGSTORYM 300
242 EAVGLPSIPVPIGTDQKLEKKGASAPPSNRKSLKVPYNGPGTNGSTORYM 301
301 HINSHETRTIYVIGTIGKAVPEPVYVILGSHQSWTGTIDRQGAAYHETVSGCT 360
302 HINSHETRTIYVIGTIGKAVPEPVYVILGSHQSWTGTIDRQGAAYHETVSGCT 361
361 LKSGPREFETILASNDAREFGLASTPNAEPNSRLQDRGVAYINADSSIEONTLYV 400
405 LKSGPREFETILASNDAREFGLASTPNAEPNSRLQDRGVAYINADSSIEONTLYV 464

361 LKSGPREFETILASNDAREFGLASTPNAEPNSRLQDRGVAYINADSSIEONTLYV 420
362 LKSGPREFETILASNDAREFGLASTPNAEPNSRLQDRGVAYINADSSIEONTLYV 421
421 DCPPLASLYVNLTELKSPDQKLEKKGASAPPSNRKSLKVPYNGPGTNGSTORYM 480
422 DCPPLASLYVNLTELKSPDQKLEKKGASAPPSNRKSLKVPYNGPGTNGSTORYM 481
481 FQGLASGRARATKMETKNSGQVLYSHVETVELKEPDMFTYVLYVQKGV 540
482 FQGLASGRARATKMETKNSGQVLYSHVETVELKEPDMFTYVLYVQKGV 541
541 PELANSYVPPQCDYAVYLYKADIVYSNKPQKMTYSVSDLSAVNPEIAS 600
542 PELANSYVPPQCDYAVYLYKADIVYSNKPQKMTYSVSDLSAVNPEIAS 601
601 FESERLOPDSNPVYVARNQOAFLEPRLTIDPLGDPFRHRYVAPSSNKTAGES 660
602 FESERLOPDSNPVYVARNQOAFLEPRLTIDPLGDPFRHRYVAPSSNKTAGES 661
661 PCTIDALFDSKTPDSKAMGKRYVAAFTVQAAETLSVA 706
662 PCTIDALFDSKTPDSKAMGKRYVAAFTVQAAETLSVA 707

Query Match 100.0% Score 706 DB 4 Length 707
Best Local Similarity 100.0% Pct. No. 0
Matches 706: Conservative 0 Mismatches 0 Indels 0 Gaps 0

3
US-08-325-553-2
Sequence 2, Application US/0832553
Patent No. 553866
GENERAL INFORMATION:
INVENTOR: 1, Ron S
APPLICANT: Heaton, Warren D. W.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
CROSS-REFERENCE TO RELATED APPLICATIONS:
ADDRESS: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/325,553
CLASSIFICATION: 435

421 DCPPLASLYVNLTELKSPDQKLEKKGASAPPSNRKSLKVPYNGPGTNGSTORYM 480
422 DCPPLASLYVNLTELKSPDQKLEKKGASAPPSNRKSLKVPYNGPGTNGSTORYM 481
481 FQGLASGRARATKMETKNSGQVLYSHVETVELKEPDMFTYVLYVQKGV 540
482 FQGLASGRARATKMETKNSGQVLYSHVETVELKEPDMFTYVLYVQKGV 541
541 PELANSYVPPQCDYAVYLYKADIVYSNKPQKMTYSVSDLSAVNPEIAS 600
542 PELANSYVPPQCDYAVYLYKADIVYSNKPQKMTYSVSDLSAVNPEIAS 601
601 FESERLOPDSNPVYVARNQOAFLEPRLTIDPLGDPFRHRYVAPSSNKTAGES 660
602 FESERLOPDSNPVYVARNQOAFLEPRLTIDPLGDPFRHRYVAPSSNKTAGES 661
661 PCTIDALFDSKTPDSKAMGKRYVAAFTVQAAETLSVA 706
662 PCTIDALFDSKTPDSKAMGKRYVAAFTVQAAETLSVA 707
705 PCTIDALFDSKTPDSKAMGKRYVAAFTVQAAETLSVA 750

Query Match 100.0% Score 706 DB 1 Length 750
Best Local Similarity 100.0% Pct. No. 0
Matches 706: Conservative 0 Mismatches 0 Indels 0 Gaps 0

US-08-394-152A-2
Sequence 2, Application US/08394152A
Patent No. 553866
GENERAL INFORMATION:
INVENTOR: 1, Ron S
APPLICANT: Heaton, Warren D. W.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
NUMBER OF SEQUENCES: 48
ADDRESS: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/394,152A
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.

REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B
TELEPHONE: (212) 378-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
LENGTH: 750
TYPE: amino acid
TOPOLOGY: linear
MOLWGT: 1524.2
DIS-194-1524-2

Query Match 100.0% Score 706; DB 2; Length 750;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SSENATITPNNKMAFLDELAKENIKFVWFOIPLACTGONFQALNKGKSPG 60
43 SSENATITPNNKMAFLDELAKENIKFVWFOIPLACTGONFQALNKGKSPG 104
61 LDEVELAHYDLASPTKTPHYISINDEGHEIFNLSLEPPPGYENSDVPPSSAF 120
105 LDEVELAHYDLASPTKTPHYISINDEGHEIFNLSLEPPPGYENSDVPPSSAF 164
121 SPOGPRDGLVYVNAARTDFPLEDMKINSGKIYARGVKGNVYANQAQAKG 180
165 SPOGPRDGLVYVNAARTDFPLEDMKINSGKIYARGVKGNVYANQAQAKG 224
181 VILXSDADYFAKVSYPGQNLKGGVQGNITLMDAGDPLPGYANETARGLA 240
225 VILXSDADYFAKVSYPGQNLKGGVQGNITLMDAGDPLPGYANETARGLA 284
241 EAVGLAPFVPIPTGTAQKLLKMGCAAPDSSRSGSLKVPYNGQTFNSTATN 300
285 EAVGLAPFVPIPTGTAQKLLKMGCAAPDSSRSGSLKVPYNGQTFNSTATN 344
301 HINSTEYTRIVYGTAKAEVDQVYILGGRDSWFGIDPGSAAVHEIYSGT 360
345 HINSTEYTRIVYGTAKAEVDQVYILGGRDSWFGIDPGSAAVHEIYSGT 404
361 LKEGMPERRITLPSNDAEFGLLSTMAENSRLLDGRVYINADSSIDETGLAV 420
405 LKEGMPERRITLPSNDAEFGLLSTMAENSRLLDGRVYINADSSIDETGLAV 464
421 DCPPLATSLVHNLTELASPDGFEKSLYESPTKSPSPFGAPRIKLSGDFEV 480
465 DCPPLATSLVHNLTELASPDGFEKSLYESPTKSPSPFGAPRIKLSGDFEV 524
481 POKLGIASGARBYETENKPSGYPVLSHYETTELKRYDPWFYLTVAQVRCGV 540

REFERENCE/DOCKET NUMBER: 8511-0013-999
TELEPHONE: (650) 493-5505
TELEFAX: (650) 493-5556
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
LENGTH: 750
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLWGT: 6150508
DIS-09-044-668-2

Query Match 100.0% Score 706; DB 3; Length 750;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SSENATITPNNKMAFLDELAKENIKFVWFOIPLACTGONFQALNKGKSPG 60
45 SSENATITPNNKMAFLDELAKENIKFVWFOIPLACTGONFQALNKGKSPG 104
61 LDEVELAHYDLASPTKTPHYISINDEGHEIFNLSLEPPPGYENSDVPPSSAF 120
105 LDEVELAHYDLASPTKTPHYISINDEGHEIFNLSLEPPPGYENSDVPPSSAF 164
121 SPOGPRDGLVYVNAARTDFPLEDMKINSGKIYARGVKGNVYANQAQAKG 180
165 SPOGPRDGLVYVNAARTDFPLEDMKINSGKIYARGVKGNVYANQAQAKG 224
181 VILXSDADYFAKVSYPGQNLKGGVQGNITLMDAGDPLPGYANETARGLA 240
225 VILXSDADYFAKVSYPGQNLKGGVQGNITLMDAGDPLPGYANETARGLA 284
241 EAVGLAPFVPIPTGTAQKLLKMGCAAPDSSRSGSLKVPYNGQTFNSTATN 300
285 EAVGLAPFVPIPTGTAQKLLKMGCAAPDSSRSGSLKVPYNGQTFNSTATN 344
301 HINSTEYTRIVYGTAKAEVDQVYILGGRDSWFGIDPGSAAVHEIYSGT 360
345 HINSTEYTRIVYGTAKAEVDQVYILGGRDSWFGIDPGSAAVHEIYSGT 404
361 LKEGMPERRITLPSNDAEFGLLSTMAENSRLLDGRVYINADSSIDETGLAV 420
405 LKEGMPERRITLPSNDAEFGLLSTMAENSRLLDGRVYINADSSIDETGLAV 464
421 DCPPLATSLVHNLTELASPDGFEKSLYESPTKSPSPFGAPRIKLSGDFEV 480
465 DCPPLATSLVHNLTELASPDGFEKSLYESPTKSPSPFGAPRIKLSGDFEV 524

541 PELANSIVLPDCEYAVLAKADKISISKHQBKATSVSPDLSFSAVKFTEIAS 600
585 PELANSIVLPDCEYAVLAKADKISISKHQBKATSVSPDLSFSAVKFTEIAS 644
601 KFSERADPKNSNPVYLAHNDQALFLEAFIDPLGDPBPYRHYIAPSSHRYAGCS 660
645 KFSERADPKNSNPVYLAHNDQALFLEAFIDPLGDPBPYRHYIAPSSHRYAGCS 704
661 POKLGIASGARBYETENKPSGYPVLSHYETTELKRYDPWFYLTVAQVRCGV 706
705 POKLGIASGARBYETENKPSGYPVLSHYETTELKRYDPWFYLTVAQVRCGV 750

RESULT 5
US-08-044-668-2
Sequence 2; Application US/09044668
Patent No. 6150508
GENERAL INFORMATION:
INVENTOR: Gerald P.
APPLICANT: Boynton, Alton L.
APPLICANT: Holmes, Eric H.
CORRESPONDENCE ADDRESS: Ethinda, LLP
STREET 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
SOFTWARE: Microsoft Windows Version 2.0b
CURRENT APPLICATION NUMBER: US/09/044,668
APPLICATION NUMBER: 6150508
FILING DATE: 08-04-1996
PRIORITY DATE: 08-04-1996
PRIORITY APPLICATION DATA:
FILING DATE: INFORMATION:
NAME: Baldwin, Geraldine F
REGISTRATION NUMBER: 31,232

481 POKLGIASGARBYETENKPSGYPVLSHYETTELKRYDPWFYLTVAQVRCGV 540
525 POKLGIASGARBYETENKPSGYPVLSHYETTELKRYDPWFYLTVAQVRCGV 584
541 PELANSIVLPDCEYAVLAKADKISISKHQBKATSVSPDLSFSAVKFTEIAS 600
585 PELANSIVLPDCEYAVLAKADKISISKHQBKATSVSPDLSFSAVKFTEIAS 644
601 KFSERADPKNSNPVYLAHNDQALFLEAFIDPLGDPBPYRHYIAPSSHRYAGCS 660
645 KFSERADPKNSNPVYLAHNDQALFLEAFIDPLGDPBPYRHYIAPSSHRYAGCS 704
661 POKLGIASGARBYETENKPSGYPVLSHYETTELKRYDPWFYLTVAQVRCGV 706
705 POKLGIASGARBYETENKPSGYPVLSHYETTELKRYDPWFYLTVAQVRCGV 750

RESULT 6
US-08-325-553-11
Sequence 11; Application US/08325553
Patent No. 5530865
GENERAL INFORMATION:
INVENTOR: Isaac, Ron S.
APPLICANT: Heaton, Warren D.W.
APPLICANT: Felt, William R.
CORRESPONDENCE ADDRESS: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
ADDRESS: Cooper & Dunham
STREET 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin release #1.0, version #1.25
CURRENT APPLICATION NUMBER: US/08/325,553
APPLICATION NUMBER: 5530865
FILING DATE: 05/07/97, 337A
PRIORITY DATE: 05 NOV 1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
FILING DATE: 05 NOV 1993
REFERENCE/DOCKET NUMBER: 31747/41426
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0523
INVENTOR: 422532 COOP UT
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
STRANDEDNESS: double
MOLECULE TYPE: linear
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORGANISM: Homo sapien
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen
US-08-325-553-11

Query Match 2.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred No. 2.6e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 656 YAGSPFQITDALPDIEST 674
DB 1 YAGSPFQITDALPDIEST 19

RESULT 7
US-08-394-152A-11
Sequence 11; Application US/08394152A
Patent No. 5935818
GENERAL INFORMATION:
APPLICANT: Israel, Ron S.
INVENTOR: Israel, Ron S.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESS: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10013
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM 310 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS

STATE: NH
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
SOFTWARE: Patent Release #1.0, Version #1.25
APPLICATION NUMBER: US/08-622,046B
FILING DATE: 26-MARCH-1996
CLASSIFICATION: 514
NAME: MOSELEY, ROBERT D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 476,001US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 339-3063
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
US-08-622-046B-21

Query Match 2.5%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred No. 2.6e-11;

QY 152 CGGATVATAGTGVFRONT 169
DB 1 CGGATVATAGTGVFRONT 18

RESULT 9
US-08-325-553-7
Sequence 7; Application US/08325553
Patent No. 558966
GENERAL INFORMATION:
APPLICANT: Israel, Ron S.
INVENTOR: Israel, Ron S.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESS: Cooper & Dunham
Street: 30 Rockefeller Plaza

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
SEQUENCE 21; Application US/08394152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 391-0520
TELEFAX: (212) 391-0520
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
STRANDEDNESS: double
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORGANISM: Homo sapien
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen
US-08-394-152A-11

Query Match 2.7%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred No. 2.6e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 656 YAGSPFQITDALPDIEST 674
DB 1 YAGSPFQITDALPDIEST 19

RESULT 8
US-08-622-046B-21
Sequence 21; Application US/08622046B
Patent No. 6103237
GENERAL INFORMATION:
APPLICANT: Israel, Ron S.
INVENTOR: Michael, Steven D.
TITLE OF INVENTION: Stable Variant HK2 Polypeptide
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Lundberg, Weesner & Kluth, P.A.
Street: P.O. Box 2036
CITY: Minneapolis

CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
SOFTWARE: Patent Release #1.0, Version #1.25
APPLICATION NUMBER: US/08-325,553
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: US/07/973,337A
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
STRANDEDNESS: double
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORGANISM: Homo sapien
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen
US-08-325-553-7

Query Match 2.4%; Score 17; DB 1; Length 22;
Best Local Similarity 100.0%; Pred No. 3.2e-10;

QY 34 TQTHLACTGTFQFLAK 50
DB 6 TQTHLACTGTFQFLAK 22

RESULT 10

US-08-394-152A-7
Sequence 7, Application US/08394152A
Patent No. 5935818
GENERAL INFORMATION:
APPLICANT: Israel, Ron S.
APPLICANT: Heaton, Warren D.W.
APPLICANT: Falt, William R., PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
TITLE OF INVENTION: US935818
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B
TELEPHONE: (212) 391-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen
US-08-394-152A-7

Query Match 2.4% Score 17: DB 2: Length 22:

MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
US-08-325-553-9

Query Match 2.3% Score 16: DB 1: Length 17:
Best Local Similarity 100.0% Predicted 66.0%
Matches 16: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 181 VLVSDPDADYFACV 196
DB 2 VLVSDPDADYFACV 17

US-08-394-152A-9
Sequence 9, Application US/08394152A
Patent No. 5935818
GENERAL INFORMATION:
APPLICANT: Israel, Ron S.
APPLICANT: Heaton, Warren D.W.
APPLICANT: Falt, William R., PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
TITLE OF INVENTION: US935818
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B

Best Local Similarity 100.0% Predicted 3.2e-10:
Matches 17: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
Qy 34 TQPHATGTONPOLAK 50
DB 6 TQPHATGTONPOLAK 22

US-08-325-553-9
Sequence 9, Application US/08325553
Patent No. 5938666
GENERAL INFORMATION:
APPLICANT: Israel, Ron S.
APPLICANT: Heaton, Warren D.W.
APPLICANT: Falt, William R., PROSTATE-SPECIFIC MEMBRANE ANTIGEN
TITLE OF INVENTION: US938666
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/325,553
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41747/41426
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 278-0400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen
US-08-394-152A-9

Query Match 2.3% Score 16: DB 2: Length 17:
Best Local Similarity 100.0% Predicted 3.2e-10:
Matches 16: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 181 VLVSDPDADYFACV 196
DB 2 VLVSDPDADYFACV 17

US-08-325-553-10
Sequence 10, Application US/08325553
Patent No. 5938666
GENERAL INFORMATION:
APPLICANT: Israel, Ron S.
APPLICANT: Heaton, Warren D.W.
APPLICANT: Falt, William R., PROSTATE-SPECIFIC MEMBRANE ANTIGEN
TITLE OF INVENTION: US938666
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/325,553

CURRENT APPLICATION DATA:
? PRIORITY NUMBER: US/08/325,553
? FILING DATE: 24-FEB-95
? CLASSIFICATION: 435
? PRIOR APPLICATION NUMBER: US/07/973,337A
? ATTORNEY/AGENT INFORMATION:
? NAME: White, John P.
? REGISTRATION NUMBER: 28,678
? TELEPHONE: (212) 977-9550
? TELEFAX: (212) 664-0525
? INFORMATION FOR SEQ ID NO: 10:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 15 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? STRANDEDNESS: double
? MOLECULE TYPE: peptide
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? ORIGIN: human
? ORGANISM: Homo sapien
? TISSUE TYPE: Carcinoma
? IMMEDIATE SOURCE:
? CLONE: Prostate Specific Membrane Antigen

Query Match 2.1% Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2,9e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 630 AFDPLDLPDPTR 644
DB 1 AFDPLDLPDPTR 15

RESULT 14
US-08-394-152A-10
? Sequence 10: Application US/08394152A
? Patent No. 5935818
? GENERAL INFORMATION:
? APPLICANT: Israel, Ron S.
? APPLICANT: Heston, Warren D.W.
? APPLICANT: Falt, William R.
? TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
? TITLE OF INVENTION: USES THEREOF

US-08-325-553-8
? Sequence 8: Application US/08325553
? Patent No. 551866
? GENERAL INFORMATION:
? APPLICANT: Israel, Ron S.
? APPLICANT: Heston, Warren D.W.
? APPLICANT: Falt, William R.
? TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
? NUMBER OF SEQUENCES: 38
? CORRESPONDENCE ADDRESSES:
? ADDRESS: Cooper & Dunham
? STREET: 30 Rockefeller Plaza
? CITY: New York
? STATE: New York
? COUNTRY: United States of America
? ZIP: 10112
? COMPUTER RELEASABLE FORM:
? MEDIUM TYPE: floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? OPERATING SYSTEM: PC-DOS/MS-DOS
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/325,553
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/07/973,337A
? ATTORNEY/AGENT INFORMATION:
? NAME: White, John P.
? REGISTRATION NUMBER: 28,678
? TELEPHONE: (212) 977-9550
? TELEFAX: (212) 664-0525
? INFORMATION FOR SEQ ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 17 amino acids
? TYPE: amino acid
? STRANDEDNESS: double
? MOLECULE TYPE: linear
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? ORIGIN: human
? IMMEDIATE SOURCE:
? CLONE: Prostate Specific Membrane Antigen

NUMBER OF SEQUENCES: 48
? CORRESPONDENCE ADDRESS:
? ADDRESS: Cooper & Dunham LLP
? STREET: 30 Rockefeller Center
? CITY: New York
? STATE: New York
? COUNTRY: United States of America
? ZIP: 10112
? COMPUTER RELEASABLE FORM:
? MEDIUM TYPE: floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? OPERATING SYSTEM: PC-DOS/MS-DOS
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/394,152A
? FILING DATE: 24-FEB-95
? ATTORNEY/AGENT INFORMATION:
? NAME: White, John P.
? REGISTRATION NUMBER: 28,678
? TELEPHONE: (212) 977-9550
? TELEFAX: (212) 391-0525
? INFORMATION FOR SEQ ID NO: 10:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 15 amino acids
? TYPE: amino acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? ORIGIN: human
? IMMEDIATE SOURCE:
? CLONE: Prostate Specific Membrane Antigen

Query Match 2.1% Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2,9e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 630 AFDPLDLPDPTR 644
DB 1 AFDPLDLPDPTR 15

RESULT 15

US-08-394-152A-8
? Sequence 8: Application US/08394152A
? Patent No. 5935818
? GENERAL INFORMATION:
? APPLICANT: Israel, Ron S.
? APPLICANT: Heston, Warren D.W.
? APPLICANT: Falt, William R.
? TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
? NUMBER OF SEQUENCES: 48
? CORRESPONDENCE ADDRESSES:
? ADDRESS: Cooper & Dunham LLP
? STREET: 185 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: United States of America
? ZIP: 10036
? COMPUTER RELEASABLE FORM:
? MEDIUM TYPE: floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? OPERATING SYSTEM: IBM 310 466 DX2
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/394,152A
? FILING DATE: 24-FEB-95
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: White, John P.
? REGISTRATION NUMBER: 28,678
? TELEPHONE: (212) 977-9550
? TELEFAX: (212) 391-0525
? INFORMATION FOR SEQ ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 17 amino acids
? TYPE: amino acid
? STRANDEDNESS: double
? TOPOLOGY: linear

MOLECULE TYPE: Peptide
AMINO ACID SEQUENCE: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Carcinoma
INVENTION TYPE: NO
CLONE: Prostate Specific Membrane Antigen
US-08-394-152A-8

Query Match 2.0%: Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 RTTLPASDAE 193
DB 1 RTTLPASDAE 14

RESULT 17
US-08-325-553-34
Sequence 34; Application US/08325533
Patent No. 5538866
GENERAL INFORMATION:
APPLICANT: Heaton, Warren D. W.
APPLICANT: Falt, William R. M.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSER: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.

MEDIUM TYPE: floppy disk
COMPUTER: IBM 310 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
NAME: White, John P.
REFERENCE/DOCKET NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 391-0520
TELEFAX: (212) 391-0523
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
STRANDEDNESS: double
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
INVENTION TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapien
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen
US-08-394-152A-34

Query Match 1.7%: Score 12; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 RTTLPASDAE 381
DB 1 RTTLPASDAE 12

RESULT 19
US-08-325-553-31
Sequence 31; Application US/08325533
Patent No. 5538866
GENERAL INFORMATION:
APPLICANT: Heaton, Warren D. W.
APPLICANT: Falt, William R. M.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
NUMBER OF SEQUENCES: 38

REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INVENTION TYPE: NO
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapien
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen
US-08-325-553-34

Query Match 1.7%: Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 RTTLPASDAE 381
DB 1 RTTLPASDAE 12

RESULT 18
US-08-394-152A-34
Sequence 34; Application US/08394152A
Patent No. 5538866
GENERAL INFORMATION:
APPLICANT: Heaton, Warren D. W.
APPLICANT: Falt, William R. M.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSER: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10105
COMPUTER READABLE FORM:

CORRESPONDENCE ADDRESS:
ADDRESSER: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,553
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REFERENCE/DOCKET NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapien
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen
US-08-325-553-31

Query Match 1.3%: Score 9; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 TDDPOLAR 50
DB 1 TDDPOLAR 9


```

1 SOFTWARE: Patientin Release #1.0, Version #1.25
2
3 CURRENT APPLICATION DATA:
4   PILING DATE: 05/06/2015.553
5   CLASSIFICATION: 435
6   PRIOR APPLICATION DATA: USC07/973.337A
7   PILING DATE: 05/06/2015.553
8   ATOMREX/AGENT INFORMATION:
9     NAME: White, John P. 26 678
10    RESIDENCE NUMBER: 1747/41426
11    TELECOMMUNICATION INFORMATION:
12      TELEPHONE: (212) 977-9550
13      TELEFAX: (212) 664 0125
14      EMAIL: jwhite@att.net
15      IMMUNIZATION FOR SEX ID NO: 6
16      SOURCE CHARACTERISTICS:
17        LENGTH: 9 amino acids
18        TYPE: alpha
19        STRANDS: double
20        TOPOLOGY: linear
21      MOLECULE TYPE: protein
22      MOLECULE WEIGHT: 9.000 kDa
23      ANTI-SENSE: NO
24
25 ORIGINAL SOURCE:
26   ORGANISM: Homo sapien
27   TISSUE: testis
28   IMMEDIATE SOURCE:
29     CLONE: Prostate Specific Membrane Antigen
30     ID: 195-08-335-553-6

```

```

Query Match      1.10; Score 8; DB 1; Length 9;
Best Local Similarity 100.00; Pred. No. 1.3e+05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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QY      311 IYNVIGTL 31E
          11111111
DB      1 IYNVIGTL 8

```

RESULT 25
US-08-394-152A-6
Sequence 6, application US/08394152A
GENERAL INFORMATION
APPLICANT: Israel, Ron S.
APPLICANT: Hesdon, Warren D.
APPLICANT: Pat, William R.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN ANT

US-08-403-803-2-copy-45_750-orig.12a

Apr 9 11:14:12 2001

RESULT: 26
US-08-793-824-2
Sequence 2: Application US/08/793824
Patent No.: 5981838
INVENTOR: GILFORD, Phillip Morrison
APPLICANT: Gilford, Phillip Morrison
APPLICANT: Jacques, Nicholas Anthony
TITLE OF INVENTION: Protection of plants to
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: Jack & Co
STREET: Level 6, 1760 Walker Street
CITY: No. 5981838th Sydney
STATE: New South Wales
COUNTRY: Australia
ZIP: 2060
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: MS-DOS/MS-PC
SOFTWARE: Patent Release \$1.0, Version 1.30
CURRENT APPLICATION DATA:
PRIORITY NUMBER: US/08/793,824
CLASSIFICATION: B00
PRIORITY APPLICATION DATA:
PILLING DATE: 24-AUG-1994
TELECOMMUNICATION INFORMATION:
TELEPHONE: 61 2 9957 5944
TELEX: 36547 2 957 6288
SEQUENCE CHARACTERISTICS:
PRIORITY FOR SEQ ID NO: 2:
TYPE: amino acids
STRANDS/GENES: 2
TOPLOGY: not relevant
NO. OF SEQUENCES: 2
ORIGINAL SOURCE: Streptococcus salivarius
ORGANISM: Streptococcus salivarius

1 TITLE OF INVENTION: USES THEREOF
 2 NUMBER OF SEQUENCES: 48
 3 CORRESPONDENCE ADDRESS: Pharm Llp
 4 STREET 1185 Avenue of the Americas
 5 CITY: New York
 6 STATE: New York
 7 COUNTRY: United States of America
 8 ZIP: 10036
 9 COMPUTER READABLE FORM:
 10 MEDIUM TYPE: Floppy disk
 11 COMPUTER: IBM 310 466 EX2
 12 SOFTWARE: IBM 310 466 EX2-POS
 13 SOFTWARE: PatentIn Release #1.0, Version 11.25
 14 CURRENT APPLICATION DATA:
 15 APPLICATION NUMBER: 05/08/394,152A
 16 FILING DATE: 04/26/95
 17 PRIORITY DATE: 04/26/95
 18 ATTORNEY/AGENT INFORMATION:
 19 NAME: White, John P.
 20 REGISTRATION NUMBER: 28,678
 21 TELECOMMUNICATION INFORMATION:
 22 TELEPHONE: (212) 278-0400
 23 TELEFAX: (212) 391-0535
 24 INFORMATION FOR SEQ ID NOS: 6:
 25 SEQUENCE CHARACTERISTICS:
 26 LENGTH: 9 amino acids
 27 TYPE: amino acid
 28 STRANDEDNESS: double
 29 MOLECULE TYPE: linear
 30 HYDROLYZABLE: NO
 31 HYDROPHILIC: NO
 32 ANTI-SENSE: NO
 33 ORIGINAL SOURCE:
 34 ORGANISM: sapien
 35 TISSUE TYPE: Carcinoma
 36 IMMEDIATE SOURCE:
 37 CLONE: Prostate Specific Membrane
 38 05-08-394-152A, 6

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Query Match      1.13; Score 8; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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QY      311 IYNVIGTL 316
        |||||
Db       1 IYNVIGTL 8
```

Mon Apr 9 11:14:12 2001

us-08-403-803-2_copy_45_750.ollg.ra

Db 1091 AFLDELKA 1098

05-08-125-553-5 APPLICATION: US/08125533
 RESULT 27
 Patent No. 5,538666
 GENERAL INFORMATION:
 APPLICANT: Iarelli, Ron S.
 INVENTOR: Iarelli, Ron S.
 APPLICANT: Patti Miller, D. M.
 TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 FILED IN: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release v1.0, Version 1.1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 06/08/93, 553
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 FILING DATE: 05/07/97, 337A
 FILING DATE: 05 Nov 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 ADDRESS: 38 578
 REFERENCE/ROCKET NUMBER: 1747/14426
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 977-9550
 TELEFAX: 432323
 COUNTRY: US
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FUNCTION: peptide
 HYDROPHILIC: NO
 ANTISENSE: NO
 ORIGINAL SOURCE:

un-08-403-803-2-copy-45-750-0119-1

un-08-403-803-2-copy-45-750-0119-1

Apr 9 11:14:11 2001

RESULT: 26

US-08-793-024-2

Sequence 2: Application US/08793824

Patent No. 5981838

GENERAL INFORMATION:

APPLICANT: Griffiths, Christine Lynn

APPLICANT: Griffith, Philip Morison

APPLICANT: Griffith, Nicholas Anthony

TITLE OF INVENTION: Genetic Manipulation of Plants to

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Griffiths Hock & Co

CITY: New South Wales

STATE: New South Wales

COUNTRY: Australia

EXP: 2010

COMPUTER: IBM PC compatible

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: GENESYS, release 11.0, version 11.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/793,824

FILING DATE: 24-AUG-1994

CLASSIFICATION: 580

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PM7643

FILING DATE: 24-AUG-1994

TELECOMMUNICATIONS INFORMATION:

TELEPHONE: 61 2 957 6388

TELEFAX: 61 2 957 6388

TELEX: 26547

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE INFORMATION:

SEQUENCE LENGTH: 1577 amino acids

TYPE: amino acid

STRANDNESS: 5' to 3'

MOLECULE TYPE: polypeptide

ORIGINAL SOURCE:

ORGANISM: Streptococcus salivarius

US-08-793-024-2

Query Match: 1.1%, Score 8, DB 2, Length 1577.

Database: GenBank, 10000, Pred. No. 26.

Matches: 0, Mismatches: 0, Indels: 0, Gaps: 0

16 APTIDEKA 23

STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER: IBM PC compatible
MEDIUM TYPE: 3.5 INCH DISKETTE
OPERATING SYSTEM: MS-DOS/MS-DOS
CURRENT APPLICATION DATA: US/08/468,847B
APPLICATION NUMBER: US/09/053,197A
CLASSIFICATION: 435
PILING DATE: 01-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: MacGill, Keith T.
REGISTRATION NUMBER: 38,210
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: DALB-01393
TELEPHONE: (415) 397-8338
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 AMINO ACIDS
TYPE: amino acids
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-468-847B-13

Query Match 1.0%; Score 7; DB 3; Length 284;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0;

OY 698 MATJES 704
DB 231 MATJES 237

RESULT 32
US-08-468-847B-13
Sequence 16, Application US/08/468,847B
Patent No. 5786263
GENERAL INFORMATION:
APPLICANT: Hastings, Gregg A. and Adam, Mark D.
TITLE OF INVENTION: Human CCR-Like G-protein Factor
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
ADDRESSEE: BECKER FARM ROAD
CITY: ROSELAND

TITLE OF INVENTION: DNA Molecules Encoding Plant
TITLE OF INVENTION: Protoporphyrinogen Oxidase and Inhibitor-Resistant Mutants
SEQUENCE 16, Application US/08/403,803
PATENT NO. 5786263
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 593602artis Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591-9005
COMPUTER: IBM PC compatible
MEDIUM TYPE: 3.5 INCH DISKETTE
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: US/08/403,803
APPLICATION NUMBER: US/08/403,803
CLASSIFICATION: 435
PILING DATE: 01-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: CGC 1847
TELEPHONE: (919) 541-8689
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 AMINO ACIDS
TYPE: amino acids
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-808-931-16

Query Match 1.0%; Score 7; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 1;e02;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

OY 102 PEPKTE 108

STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07066
COMPUTER: IBM PC compatible
MEDIUM TYPE: 3.5 INCH DISKETTE
OPERATING SYSTEM: MS-DOS/MS-DOS
CURRENT APPLICATION DATA: US/08/468,847B
APPLICATION NUMBER: US/08/468,847B
CLASSIFICATION: 435
PILING DATE: 6 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: MacGill, Keith T.
REGISTRATION NUMBER: 38,210
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 325800-442
TELEPHONE: (415) 397-8338
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 AMINO ACIDS
TYPE: amino acids
STRANDEDNESS: not relevant
TOPOLOGY: LINDAR
MOLECULE TYPE: PROTEIN
US-08-468-847B-13

Query Match 1.0%; Score 7; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

OY 454 TRKSPSP 460
DB 284 TRKSPSP 290

RESULT 33
US-08-808-931-16
Sequence 16, Application US/08/808,931
Patent No. 5786263
GENERAL INFORMATION:
APPLICANT: Voizeth, Sandra
TITLE OF INVENTION: Protoporphyrinogen Oxidase Genes
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018105artis Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591-9005
COMPUTER: IBM PC compatible
MEDIUM TYPE: 3.5 INCH DISKETTE
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: US/08/808,931
APPLICATION NUMBER: US/08/808,931
CLASSIFICATION: 800
PILING DATE: 28-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: CGC 1846
TELEPHONE: (919) 541-8689
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 AMINO ACIDS
TYPE: amino acids

US-08-808-931-16
Sequence 16, Application US/08/808,931
Patent No. 5786263
GENERAL INFORMATION:
APPLICANT: Johnson, Marie
TITLE OF INVENTION: Protoporphyrinogen Oxidase Genes
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018105artis Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591-9005
COMPUTER: IBM PC compatible
MEDIUM TYPE: 3.5 INCH DISKETTE
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: US/08/808,931
APPLICATION NUMBER: US/08/808,931
CLASSIFICATION: 800
PILING DATE: 28-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: CGC 1846
TELEPHONE: (919) 541-8689
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 AMINO ACIDS
TYPE: amino acids

STRANDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-403-803-2-copy_45_750.o11g.txt

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 539;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 102 PEPGYE 108
DB 187 PEPGYE 193

RESULT 35
US-09-050-603A-16
US-09-050-603A-16 Application US/09050603A
Patent No. 6021012
GENERAL INFORMATION:
APPLICANT: Volinath, Sandra
APPLICANT: Johnson, Marie
APPLICANT: Johnson, Marie
APPLICANT: Hefetz, Peter
APPLICANT: Hefetz, Peter
TITLE OF INVENTION: DNA Molecules Encoding Plant
PROTEIN ENDOGENOUSLY EXPRESSED BY PLANT
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 6021012, Artia Corporation
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050/603A
FILING DATE: 30-MAR-1998
CLASSIFICATION: B00
PRIOR APPLICATION DATA: US 09/080,931
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA: US 60/012,705
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102/4208
FILING DATE: 22-JUN-1998
CLASSIFICATION: B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/059,164
FILING DATE: 13-APR-1998
PRIOR APPLICATION DATA: US 09/050,603
FILING DATE: 30-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/126,430
FILING DATE: 11-MAR-1998
PRIOR APPLICATION DATA: US 08/808,931
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA: US 60/012,705
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,612
FILING DATE: 11-FEB-1996
PRIOR APPLICATION DATA: US 60/020,003
FILING DATE: 21-JUN-1996
PRIOR APPLICATION DATA: US 08/472,028
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heiga, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 amino acids
TYPE: amino acid
STRANDNESS: not relevant
MOLECULE TYPE: protein
US-09-102-4208-16

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 539;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICATION NUMBER: US 60/013,612
FILING DATE: 11-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,003
FILING DATE: 21-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Heiga, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 amino acids
TYPE: amino acid
STRANDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-050-603A-16

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 539;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 102 PEPGYE 108
DB 187 PEPGYE 193

RESULT 36
US-09-102-4208-16
US-09-102-4208-16 Application US/091024208
Patent No. 6084155
GENERAL INFORMATION:
APPLICANT: Volinath, Sandra
APPLICANT: Johnson, Marie
APPLICANT: Johnson, Marie
APPLICANT: Hefetz, Peter
APPLICANT: Hefetz, Peter
TITLE OF INVENTION: HERBICIDE-TOLERANT PROTOPHYTIN
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 6084155, Artia Corporation
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/547,197
FILING DATE: 08-547,197
ATTORNEY/AGENT INFORMATION:
NAME: Rogalsky, Peter
REGISTRATION NUMBER: 38,601
REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)
TELEPHONE: (716) 263-1634
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
US-08-547,197-1

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 622;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 GLRSPV 250
DB 190 GLRSPV 196

RESULT 38
US-08-957-940-1

Sequence 1, Application US/08957940
GENERAL INFORMATION:
APPLICANT: Gonsky, Joseph K.
TITLE OF INVENTION: A METHOD FOR DETECTING A MANUAL'S PRIOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Clinton Square, P.O. Box 1051
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.10
APPLICATION NUMBER: US/08/957,940
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PUBLICATION NUMBER: US/08/547,197
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Rosaleny, Peter
REGISTRATION NUMBER: 39,601
TELEPHONE: (716) 263-1634
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 DELAAE 24
DB 1 DELAAE 6

RESULT 40
US-08-325-553-36

Sequence 36, Application US/08325553
GENERAL INFORMATION:
APPLICANT: Heaton, Warren D. W.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESS: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/325,553
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 GLRSPV 250
DB 190 GLRSPV 196

RESULT 39
US-08-325-553-35

Sequence 35, Application US/08325553
GENERAL INFORMATION:
APPLICANT: Heaton, Warren D. W.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESS: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10112
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/325,553
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PUBLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9550
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
ANTHROPIC: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapien
CELL TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 MEDGE 93
DB 1 MEDGE 6

RESULT 41
US-08-325-553-37

Sequence 37, Application US/08325553
GENERAL INFORMATION:
APPLICANT: Heaton, Warren D. W.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESS: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/325,553
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/325,553
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
PRIORITY/AGENT INFORMATION:
APPLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: Heaton, Warren D. M.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/41426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 664-0400
TELEFAX: (212) 664-0520
TELEX: 422523 COOP UT
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
CELL TYPE: Homo sapien
Tissue: Prostate
IMMEDIATE SOURCE:
US-08-325-553-37

Query Match 0.84; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred No. 1,3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 KSPDB06 443
|||||
DB 1 KSPDB06 6

RESULT 42
US-08-394-152A-35
Sequence 35, Application US/08394152A

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Page 71

QY 19 DELTA 24
|||||
DB 1 DELTA 6

RESULT 43
US-08-394-152A-36
Sequence 36, Application US/08394152A

GENERAL INFORMATION:
PATENT NO. 5935818
APPLICANT: Heaton, Warren D. M.
INVENTOR: Heaton, Warren D. M.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
METHOD OF INVENTION: US25 THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
NAME: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
PRIORITY/AGENT INFORMATION:
APPLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/41426-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 191-0525
TELEX: 422523 COOP UT
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
CELL TYPE: Homo sapien
Tissue: Prostate
IMMEDIATE SOURCE:
US-08-394-152A-36

PATENT NO. 5935818
GENERAL INFORMATION:
PATENT NO. 5935818
APPLICANT: Heaton, Warren D. M.
INVENTOR: Heaton, Warren D. M.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
METHOD OF INVENTION: US25 THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
NAME: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
PRIORITY/AGENT INFORMATION:
APPLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/41426-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 191-0525
TELEX: 422523 COOP UT
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
CELL TYPE: Homo sapien
Tissue: Prostate
IMMEDIATE SOURCE:
US-08-394-152A-35

Query Match 0.84; Score 6; DB 2; Length 6;
Best Local Similarity 100.0%; Pred No. 1,3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mon Apr 9 11:14:12 2001 us-08-403-803-2_copy_45_750.olly.rsl

Page 72

CELL TYPE: Carcinoma
IMMEDIATE SOURCE:
US-08-394-152A-36

Query Match 0.84; Score 6; DB 2; Length 6;
Best Local Similarity 100.0%; Pred No. 1,3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 MEDC 93
|||||
DB 1 MEDC 6

RESULT 44
US-08-394-152A-37
Sequence 37, Application US/08394152A

GENERAL INFORMATION:
PATENT NO. 5935818
APPLICANT: Heaton, Warren D. M.
INVENTOR: Heaton, Warren D. M.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
METHOD OF INVENTION: US25 THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
NAME: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
PRIORITY/AGENT INFORMATION:
APPLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/41426-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 191-0525
TELEX: 422523 COOP UT
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
CELL TYPE: Homo sapien
Tissue: Prostate
IMMEDIATE SOURCE:
US-08-394-152A-37

LENGTH: 6 amino acids
TYPE: amino acid
STRANDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
PROTEIN TYPE: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapien
CELL TYPE: Carcinoma
INSTRUMENT: 8 amino acids
CLONE: Prostate Specific Membrane Antigen
US-08-394-152A-37

Query Match
Best Local Similarity 100.0%
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 438 KSPD6 443
DB 1 KSPD6 6

RESULT 45
US-07-968-781A-12
Sequence 12, Application US/07968781A
Patent No. 5430137

GENERAL INFORMATION:
APPLICANT: Schmeffel, Frank H.
ATTORNEY/AGENT INFORMATION:
APPLICANT: Thompson, Mark
APPLICANT: Schmeffel, H. Ernest
APPLICANT: Schmeffel, George E.
TITLE OF INVENTION: Method for the identification of Bacillus
TITLE OF INVENTION: Huntington's Endotoxin Genes
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
STREET: 2401 N.W. 1st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25

OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible
APPLICATION NUMBER: PCCT/0592/10068
FILING DATE: 19921120
CLASSIFICATION:
PRIOR APPLICATION DATA:
REGISTRATION NUMBER: US 07/798, 221
FILING DATE: 22-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: SCR221P
FILING DATE: 22-NOV-1991
TELEPHONE: 619-554-2837
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
PROTEIN TYPE: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Region
CELL TYPE: Region
INSTRUMENT: Region
CLONE: Region
OTHER INFORMATION: /note: "Added amino-terminal
OTHER INFORMATION: /note: "Added carboxy-terminal
OTHER INFORMATION: /note: "Added residue"
PCT-US93-10068-4

Query Match
Best Local Similarity 100.0%
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 442 KSPD6 447
DB 3 KSPD6 8

RESULT 47
US-08-305-871A-28
Sequence 12, Application US/08305871A
Patent No. 5736142

APPLICATION NUMBER: US/07/968, 781A
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Salviach, David R.
REGISTRATION NUMBER: 21,744,444, PNOCI
FILING DATE: 14-SEP-1993
TELEPHONE: 904-375-8100
TELEFAX: 904-375-8800
INSTRUMENT: 8 amino acids
CLONE: 8 amino acids
OTHER INFORMATION: /note: "Added amino-terminal
OTHER INFORMATION: /note: "Added carboxy-terminal
OTHER INFORMATION: /note: "Added residue"
PCT-US93-10068-4

Query Match
Best Local Similarity 100.0%
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 286 KSPD6 291
DB 1 KSPD6 6

GENERAL INFORMATION:
APPLICANT: Alletti, Dario C
ATTORNEY/AGENT INFORMATION:
APPLICANT: Thompson, Mark
APPLICANT: Schmeffel, H. Ernest
APPLICANT: Schmeffel, George E.
TITLE OF INVENTION: Factor X-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
STREET: 2401 N.W. 1st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.30

GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
ATTORNEY/AGENT INFORMATION:
APPLICANT: Schmeffel, H. Ernest
APPLICANT: Schmeffel, George E.
TITLE OF INVENTION: Alteration of Immune Response Using Pan
TITLE OF INVENTION: Anti-Binding Peptides
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
STREET: Two Embroidery Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: PCCT/0592/10068
FILING DATE: 14-SEP-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA: US 08/121,101
REGISTRATION NUMBER: 21,744,444, PNOCI
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 24,744,117-0062-10
FILING DATE: 14-SEP-1993
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0100
INSTRUMENT: 8 amino acids
CLONE: 8 amino acids
OTHER INFORMATION: /note: "Added amino-terminal
OTHER INFORMATION: /note: "Added carboxy-terminal
OTHER INFORMATION: /note: "Added residue"
PCT-US93-10068-4

Query Match
Best Local Similarity 100.0%
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 286 KSPD6 291
DB 1 KSPD6 6

RESULT 48
US-08-305-871A-28
Sequence 12, Application US/08305871A
Patent No. 5736142

Best Local Similarity 100.0%; Pred No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 697 AAERTL 702
DB 4 AAERTL 9

RESULT 48
US-08-47-5098-112
SEQUENCE: 1 Application US/08164618
GENERAL INFORMATION:
PATENT: Patent No. 5408036
APPLICANT: GMAHILL, M. REZA
TITLE OF INVENTION: Peptides and Synthetic Methods
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESS: Dresser, Goldsmith, Shore, Sukter &
STREET: 180 No. 5408036th Stearns, Suite 4700
CITY: Chicago
STATE: Illinois
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SOFTWARE: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,618
FILING DATE: 05/07/1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/551,988
FILING DATE: 05/07/1993
ATTORNEY/AGENT INFORMATION:
NAME: Gerson, Edward G.
REGISTRATION NUMBER: 29,381
TELEPHONE: (312) 616-5400
TELEFAX: (312) 616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear

SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-156-552A-8
Query Match 0.8%; Score 6; DB 1; Length 16;
Best Local Similarity 100.0%; Pred No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 258 AGLTLE 263
DB 3 AGLTLE 8

RESULT 50
US-08-47-5098-112
SEQUENCE: 1 Application US/08475098
GENERAL INFORMATION:
PATENT: Patent No. 5770697
APPLICANT: Ferrari, Franco A
TITLE OF INVENTION: Peptides and Synthetic Methods
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESS: Dresser, Goldsmith, Shore, Sukter &
STREET: 180 No. 5408036th Stearns, Suite 4700
CITY: Chicago
STATE: Illinois
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SOFTWARE: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,5098
FILING DATE: 05/08/1993
CLASSIFICATION: 435-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 05/08/1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993

MOLECULE TYPE: peptide
US-08-164-618-1
Query Match 0.8%; Score 6; DB 1; Length 15;
Best Local Similarity 100.0%; Pred No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 258 AGLTLE 263
DB 3 AGLTLE 8

RESULT 49
US-08-156-552A-6
SEQUENCE: 1 Application US/08156552A
GENERAL INFORMATION:
PATENT: Patent No. 5761555
APPLICANT: Bokoch, Gary M
TITLE OF INVENTION: Peptides and Synthetic Methods
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESS: The Scripps Research Institute, Office of
STREET: 10666 No. 5761555th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SOFTWARE: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/156,552A
FILING DATE: 02-AUG-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Trepcartin, Richard P.
REGISTRATION NUMBER: 31,801
TELEPHONE: (415) 554-6112
TELEFAX: (415) 554-6112
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear

PRIOR APPLICATION DATA:
FILING DATE: 28-OCT-1987
APPLICATION NUMBER: US 06/927,258
FILING DATE: 08-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trepcartin, Richard P.
REGISTRATION NUMBER: 31,801
TELEPHONE: (415) 554-6112
TELEFAX: (415) 554-6112
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-47-5098-112

Query Match 0.8%; Score 6; DB 1; Length 21;
Best Local Similarity 100.0%; Pred No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 523 DPEKTY 528
DB 1 DPEKTY 6

Search completed: April 6, 2001, 16:56:59
Job time: 133 sec


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960 6 0 8 508 18 M35712 Terebinth flavonoid
961 6 0 8 508 18 M35711 Chrysanthemum flavonoid
962 6 0 8 508 20 Y29467 Human secreted prot
963 6 0 8 510 20 Y08862 A. gossypii glutam
964 6 0 8 512 18 M35702 Rice hexose carboxe
965 6 0 8 512 18 M35700 Rice hexose carboxe
966 6 0 8 513 18 M35710 Rose flavonoid 3'-
967 6 0 8 517 18 M35713 Japanese morning gl
968 6 0 8 518 13 R27544 Human calcium chan
969 6 0 8 519 18 M20640 M. tuberculosis
970 6 0 8 519 18 M20640 M. tuberculosis
971 6 0 8 520 17 R88426 Arabidopsis thaliana
972 6 0 8 523 19 M78006 Trimeric FliJ-G-C
973 6 0 8 523 19 M78006 Trimeric FliJ-G-C
974 6 0 8 527 18 M08167 RSV trimeric N
975 6 0 8 527 20 Y14288 Mycobacterium spec
976 6 0 8 527 20 Y14288 Mycobacterium spec
977 6 0 8 527 20 Y14288 Mycobacterium spec
978 6 0 8 527 20 Y14288 Mycobacterium spec
979 6 0 8 536 19 M61332 M. tuberculosis
980 6 0 8 536 19 M61332 M. tuberculosis
981 6 0 8 536 19 M61332 M. tuberculosis
982 6 0 8 536 19 M61332 M. tuberculosis
983 6 0 8 536 19 M61332 M. tuberculosis
984 6 0 8 537 20 M88463 Bacillus anthracis
985 6 0 8 540 19 M70460 South African Atho
986 6 0 8 540 19 M70460 Sindbis virus npr1
987 6 0 8 540 19 M70460 Sindbis virus npr1
988 6 0 8 540 19 M70460 Sindbis virus npr1
989 6 0 8 544 19 M78116 Human FtsZ repress
990 6 0 8 548 18 M07700 Human FtsZ repress
991 6 0 8 548 20 Y02535 ICAM-6 protein ap1
992 6 0 8 548 20 Y02535 ICAM-6 protein ap1
993 6 0 8 548 20 Y02535 ICAM-6 protein ap1
994 6 0 8 552 20 M03172 Human heart muscle
995 6 0 8 553 20 Y55721 Human forkhead tra
996 6 0 8 553 20 Y55721 Human forkhead tra
997 6 0 8 553 20 Y55721 Human forkhead tra
998 6 0 8 553 20 Y55721 Human forkhead tra
999 6 0 8 554 19 R04460 Human FRAC3 protei
1000 6 0 8 554 19 R04460 Human FRAC3 protei
1000 6 0 8 555 18 M28503 A. oryzae ATCC2038
Timothy grass poll
```

ALIGNMENTS

```
SEQUENCE 1
M47155 standard: Protein: 707 AA.
XX M47155:
AC M47155:
```

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```
Best Local Similarity: 100.0%; Pred. No. 0;
Matches: 706; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0.
```

```
0Y 1 SSSSTATTTPHHHKAFLDLELAENIKFPLVPTQIPHLACTQNFOLAKIOISQENFG 60
Db 2 SSSSTATTTPHHHKAFLDLELAENIKFPLVPTQIPHLACTQNFOLAKIOISQENFG 61
0Y 61 LQSVLEAHYDVLSTPNTKTPNTSTIENQGNZPTNLSFPPPPYENVEDIVPPSNP 120
Db 61 LQSVLEAHYDVLSTPNTKTPNTSTIENQGNZPTNLSFPPPPYENVEDIVPPSNP 121
0Y 121 SPQGPBGLVYVNAFEDPFTLEENKINCSGKIVARIGVPRGNKYNAQAGAG 180
Db 121 SPQGPBGLVYVNAFEDPFTLEENKINCSGKIVARIGVPRGNKYNAQAGAG 181
0Y 181 VILESDPADYFAVAKSPCKNLDGCGNGLNGLNAGADPPGTPANETARFICIA 240
Db 181 VILESDPADYFAVAKSPCKNLDGCGNGLNGLNAGADPPGTPANETARFICIA 241
0Y 241 BAVGLSPHPNPTGYDAKGLFPGKGAAPPSNNGSLAVYVNGKPGNPTSGKIV 300
Db 241 BAVGLSPHPNPTGYDAKGLFPGKGAAPPSNNGSLAVYVNGKPGNPTSGKIV 301
0Y 301 HINSHNRTATRYVTCRGAVPDPVYVLCGRSGPGGCTDROSAVNHENYSGCT 360
Db 301 HINSHNRTATRYVTCRGAVPDPVYVLCGRSGPGGCTDROSAVNHENYSGCT 361
0Y 361 LKSGRPARTITANANERELGASTNENKSLDGRGVATINDSIEGNTLRF 420
Db 361 LKSGRPARTITANANERELGASTNENKSLDGRGVATINDSIEGNTLRF 421
0Y 421 DCTPLATSLVNNLTNLSAPDPRKPKALVESWTKEPSPFGSNPRISKSGNFEVF 480
Db 421 DCTPLATSLVNNLTNLSAPDPRKPKALVESWTKEPSPFGSNPRISKSGNFEVF 481
0Y 481 PQLGLASGAAATKMTNKGSGYPLNHYVETELVKKYDPWFVYLVAVQNGGV 540
Db 481 PQLGLASGAAATKMTNKGSGYPLNHYVETELVKKYDPWFVYLVAVQNGGV 541
0Y 541 PELANSIYLPFCQADYAVARVADRTYSINHHQDRTSVSPDLSFVSNFELAS 600
Db 541 PELANSIYLPFCQADYAVARVADRTYSINHHQDRTSVSPDLSFVSNFELAS 601
0Y 601 KESERLQDFKSNPTVPLHMMNQAFLEKAPFDPGLDPPRFRRVYVAPSHNKAES 660
Db 601 KESERLQDFKSNPTVPLHMMNQAFLEKAPFDPGLDPPRFRRVYVAPSHNKAES 661
0Y 661 PCGTALDPTSGVDPKANGVKEOIVYAAFTVOAALETSPA 706
Db 661 PCGTALDPTSGVDPKANGVKEOIVYAAFTVOAALETSPA 707
```

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```
XX 28-MAR-1998 (first entry)
XX Extracellular domain of prostate specific membrane antigen (PSMA).
DE FC region: immunoglobulin, recombinant DNA, target protein: PSMA.
XX Extracellular domain of prostate specific membrane antigen, immunofusin.
XX extracellular domain.
OS Homo sapiens.
XX US5726044-A.
XX 10-MAR-1998.
XX 14-SEP-1995: 9505-052812.
XX 14-SEP-1995: 9505-052812.
XX 14-SEP-1994: 9405-030570.
XX (FUT-) FURT IMMUNOPHARMACEUTICALS CORP.
XX Gilles SD, Lo K, Sudo Y.
XX WPI: 1998-192768/17.
XX Recombinant DNA for expression of target protein, e.g. HIV gp120 -
XX PT complements sequences coding for signal peptide, immuno-globulin Fc
XX region and gp120
XX Example 14, columns 27-32, 18pp; English
XX This is the extracellular domain of the prostate specific membrane
XX antigen (PSMA) which is a type II membrane protein. The extracellular
XX domain of PSMA is a type II membrane protein. The extracellular
XX PSMA immunofusin. The recombinant DNA construct encodes the
XX expression and secretion of a target protein, whose sequence is free of
XX immunoglobulin CH1 domain. The construct comprises a polynucleotide
XX encoding from its 5' to 3' direction a secretion signal sequence,
XX sequence encoding the target protein. A replicable expression vector,
XX comprising the polynucleotide sequence can be used to transfect a host
XX cell. The products can be used to produce a recombinant fusion protein
XX (immunofusin) comprising the Fc region and target protein. The DNA can
XX be used to produce a recombinant fusion protein, and the fusion protein is
XX efficiently produced and secreted.
XX Sequence 707 AA.
```

Query Match 100.0%; Score 706; DB 19; Length 707;

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```
SEQUENCE 2
Y84667 standard: Protein: 741 AA.
XX Y84667:
XX 25-JUL-2000 (first entry)
XX Amino acid sequence of a human prostate specific membrane antigen.
XX Human, prostate specific membrane antigen, inactive antigen, cancer.
XX Prostate cancer.
XX Homo sapiens.
XX M0200010933-A1.
XX 06-APR-2000.
XX 09-SEP-1999: 99NO-0520506.
XX 30-SEP-1998: 98US-0154034.
XX (AMT-) AMERICAN FOUND BIOLOGICAL RES INC.
XX (MURK-) MURKOFF M S.
XX (LOUK-) LOUKOV D I.
XX (ZOB-) ZOBAN S.
XX Mincheff MS, Loukinov DI, Zoubak S.
XX WPI: 2000-293166/25.
XX N-PDB: A12732.
XX New DNA constructs expressing functionally inactive, altered antigens
XX are used for treating prostate cancer.
XX Disclosure: Page 16-18; 23pp; English.
XX The present sequence represents a human prostate specific membrane
XX antigen. The polynucleotide is used to construct the DNA constructs of
XX the invention. The specification describes DNA constructs which cause
XX expression of functionally inactive, altered antigens which are
XX immunofusins. The polynucleotide sequence encodes the amino acid
XX translation of DNA, translation of RNA or the expression of antigenic
XX peptides. RNA or plasmid DNA constructs encoding the extracellular
XX portion of human prostate specific membrane antigen are used for
XX treating cancer and specifically prostate cancer. The constructs can
XX be used to produce a recombinant fusion protein, and the fusion protein is
XX efficiently produced and secreted.
XX functionally active molecules being secreted or expressed on the
```

CC membrane of transfected cells. The transfection causes dendritic cells
CC to present an antigen derived from prostate cancer cells on their
CC surface.
XX
XX Sequence 741 AA:

Query Match 100.0% Score 706; DB 21; Length 741:

Best Local Similarity 100.0%; Pred. No. 0;
Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSMETNTPRNNKALFADLAKANITKFTVWFOPLHAGTROMKQLOKOTSGHENG 60
DB 3 aeneetclphmaafidclkaenlkftlyfcpqlkqfcmqlaklqdvvefy 62
QY 63 LDEGLAVDTLSTRTKTPRTISTINDEKMEFRTSLPEPPPGCTGVNDLTPPNSAF 120
DB 63 LDEGLAVDTLSTRTKTPRTISTINDEKMEFRTSLPEPPPGCTGVNDLTPPNSAF 122
QY 121 SPQKPDQVLYVWARTPEPRLERDNKJNCSKIVYANGKVRKCNVKNQAAG 180
DB 121 SPQKPDQVLYVWARTPEPRLERDNKJNCSKIVYANGKVRKCNVKNQAAG 182
QY 183 VILYSDADYPAKVSPPQGNLPGCGVRCNTILMAKADPLPCYPAHEATAREGIA 240
DB 183 VILYSDADYPAKVSPPQGNLPGCGVRCNTILMAKADPLPCYPAHEATAREGIA 242
QY 241 BAVGLPSIPWPGTGYDAQKLEHMGCAPOSSNGSLKVPYNGCPCTGNSPQVEM 300
DB 241 BAVGLPSIPWPGTGYDAQKLEHMGCAPOSSNGSLKVPYNGCPCTGNSPQVEM 302
QY 301 HHSNTEVTRIVYGLTAKGAVEDRYVILGCRDSWFCGIDPGCAVYNEIYSPCT 360
DB 301 HHSNTEVTRIVYGLTAKGAVEDRYVILGCRDSWFCGIDPGCAVYNEIYSPCT 362
QY 361 LAKESQPHARTILFASNDAPRGLASTPAENKSLQGRVYANLDSITGHTTAV 420
DB 361 LAKESQPHARTILFASNDAPRGLASTPAENKSLQGRVYANLDSITGHTTAV 422
QY 421 DCPHAGSIVNKLTELSADQDTRGKSLVSKKSPSPESQAPRTSLKCGNDPPE 480
DB 421 DCPHAGSIVNKLTELSADQDTRGKSLVSKKSPSPESQAPRTSLKCGNDPPE 482
QY 481 FQNLASQARTNMTNENKSPPLYSVETTELTEKPTDMEKTLVYAVNGCAV 540
DB 481 FQNLASQARTNMTNENKSPPLYSVETTELTEKPTDMEKTLVYAVNGCAV 542
QY 541 PELANSIVLPDGRVAVLAKADKISIKKIPDARKTSVDFLSAVKNTSTIAS 600
DB 541 PELANSIVLPDGRVAVLAKADKISIKKIPDARKTSVDFLSAVKNTSTIAS 602

PT useful for identifying haematogenous micro-metastatic tumour cells
PT and for identifying ligand which bind to PSN Ag
XX
XX Claim 24: Page 103-106; 196pp: English.

CC R55097 is a prostate specific membrane antigen (PSM, encoded by
CC Q56530). The inventors have identified a peptide of high In the
CC protein, the amino acid residue 19 to residue 44. The PSM coding sequence
CC from amino acid residue 19 to residue 44. The PSM coding sequence
CC is useful for suppressing or modulating the metastatic ability of
CC prostate tumor cells to grow, or for eliminating them. The protein
CC is useful for suppressing or modulating the metastatic ability of
CC attractive target for Ab-directed imaging and targeting of prostate
CC tumour deposits.
XX
XX Sequence 750 AA:

Query Match 100.0% Score 706; DB 15; Length 750:

Best Local Similarity 100.0%; Pred. No. 0;
Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSMETNTPRNNKALFADLAKANITKFTVWFOPLHAGTROMKQLOKOTSGHENG 60
DB 45 aeneetclphmaafidclkaenlkftlyfcpqlkqfcmqlaklqdvvefy 104
QY 61 LDEGLAVDTLSTRTKTPRTISTINDEKMEFRTSLPEPPPGCTGVNDLTPPNSAF 120
DB 105 LDEGLAVDTLSTRTKTPRTISTINDEKMEFRTSLPEPPPGCTGVNDLTPPNSAF 164
QY 121 SPQKPDQVLYVWARTPEPRLERDNKJNCSKIVYANGKVRKCNVKNQAAG 180
DB 165 SPQKPDQVLYVWARTPEPRLERDNKJNCSKIVYANGKVRKCNVKNQAAG 224
QY 181 VILYSDADYPAKVSPPQGNLPGCGVRCNTILMAKADPLPCYPAHEATAREGIA 240
DB 225 VILYSDADYPAKVSPPQGNLPGCGVRCNTILMAKADPLPCYPAHEATAREGIA 284
QY 241 BAVGLPSIPWPGTGYDAQKLEHMGCAPOSSNGSLKVPYNGCPCTGNSPQVEM 300
DB 285 BAVGLPSIPWPGTGYDAQKLEHMGCAPOSSNGSLKVPYNGCPCTGNSPQVEM 344
QY 301 HHSNTEVTRIVYGLTAKGAVEDRYVILGCRDSWFCGIDPGCAVYNEIYSPCT 360
DB 345 HHSNTEVTRIVYGLTAKGAVEDRYVILGCRDSWFCGIDPGCAVYNEIYSPCT 404
QY 361 LAKESQPHARTILFASNDAPRGLASTPAENKSLQGRVYANLDSITGHTTAV 420
DB 405 LAKESQPHARTILFASNDAPRGLASTPAENKSLQGRVYANLDSITGHTTAV 464

QY 601 KPSRLQDFKSNPVLBNKQDLPLERAFIDPLDPPRTYVAPSSHNKTAGSS 660
DB 603 KPSRLQDFKSNPVLBNKQDLPLERAFIDPLDPPRTYVAPSSHNKTAGSS 662
QY 661 FPGYDALPDIKSDVPSAKKQRTYVAFVQAALSTISVA 706
DB 663 FPGYDALPDIKSDVPSAKKQRTYVAFVQAALSTISVA 708

RESULT 3
R55097 standard; Protein: 750 AA.

XX R55097.
AC R55097.

XX 11-MAR-1995 (first entry)
DE Prostate-specific membrane antigen.

XX Prostate-specific membrane antigen; PSM; prostate cancer;
XX antigen; human; 5150; protein; imaging; targeting; tumour detection;
XX antibody detection.

XX Homo sapiens.

XX Key

XX Peptide

XX Peptide

XX Peptide

XX Domain

XX M09409820-A.

XX 11-MAR-1994.

XX 05-NOV-1993; 93MO-US10624.

XX 05-NOV-1992; 92US-0973337.

XX (SIOR) SLOAN KETTERING INST CANCER.

XX FALF WR, Heston MDW, Israeli RS;

XX WPI: 1994-167129/20.

XX N-PDB: Q65520.

XX Prostate-specific membrane antigen and DNA encoding it - 16

QY 421 DCPHAGSIVNKLTELSADQDTRGKSLVSKKSPSPESQAPRTSLKCGNDPPE 480
DB 465 DCPHAGSIVNKLTELSADQDTRGKSLVSKKSPSPESQAPRTSLKCGNDPPE 524
QY 481 FQNLASQARTNMTNENKSPPLYSVETTELTEKPTDMEKTLVYAVNGCAV 540
DB 525 FQNLASQARTNMTNENKSPPLYSVETTELTEKPTDMEKTLVYAVNGCAV 584
QY 541 PELANSIVLPDGRVAVLAKADKISIKKIPDARKTSVDFLSAVKNTSTIAS 600
DB 585 PELANSIVLPDGRVAVLAKADKISIKKIPDARKTSVDFLSAVKNTSTIAS 644
QY 601 KPSRLQDFKSNPVLBNKQDLPLERAFIDPLDPPRTYVAPSSHNKTAGSS 660
DB 645 KPSRLQDFKSNPVLBNKQDLPLERAFIDPLDPPRTYVAPSSHNKTAGSS 704
QY 661 FPGYDALPDIKSDVPSAKKQRTYVAFVQAALSTISVA 706
DB 705 FPGYDALPDIKSDVPSAKKQRTYVAFVQAALSTISVA 750

RESULT 4
K41074
ID K41074 standard; protein: 750 AA.
XX K41074.
AC K41074.
XX 09-DEC-1999 (first entry)
DE PSMa extracellular domain fragment.
XX PSMa, prostate specific membrane antigen; PSM; protein; prostate cancer;
XX Homo sapiens.
XX M09407554-A1.
XX 23-SEP-1999.
XX 18-MAR-1999; 99MO-US05864.
XX 18-MAR-1998; 98US-0044668.
XX (NBI-) NORTHWEST BIOTHEAPROTICS INC.
XX Murphy GP, Boynton AU, Holmes RH, Tiao WT;
XX WPI: 1999-580294/49.
XX New monoclonal antibodies, for diagnosis and treatment of prostate

[illegible][illegible]

RESULT	5
PROT	
ID	Y92619 standard; Protein: 750 AA.
XX	
XX	
XX	Y92619:
XX	
DT	10-MOS-2000 (first entry)
XX	
XX	Human prostate specific membrane antigen.
XX	
XX	Prostate specific membrane antigen; splice variant; vaccination;
XX	Cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer;
XX	Prostate cancer; cell-associated peptide antigen; foreign epitope.
OS	Homo sapiens.
XX	
XX	Key
XX	Location/Qualifiers
XX	58-750
FT	'label' PSW
ET	

P1	Domain	/note="splice variant"
P2		1. 19
P3	Region	/label= cytoplasmic
P4		/label= antibody binding region
P5		/note="experimentally found B cell epitope"
P6	Peptide	4. 12
P7		/label= Epitope
P8		16. 52
P9	Region	/label= subdominant CTL epitope"
P10		/note="suitable for foreign T helper epitope insertion"
P11	Domain	20. 43
P12		/label= Transmembrane
P13	Disulfide-bond	22
P14		/note="preserved in immunogenised constructs"
P15	Domain	44. 750
P16		/label= B intracellular
P17	Region	63. 69
P18		/label= antibody binding region
P19		/note="computer-predicted antigenic determinant"
P20	Region	/label= antibody binding region
P21		/note="experimentally found B cell epitope"
P22	Region	87. 108
P23		/label= insertion region
P24	Region	132. 137
P25		/note="suitable for foreign T helper epitope insertion"
P26	Region	/label= antibody binding region
P27		/note="experimentally found B cell epitope"
P28	Region	132. 137
P29		/label= antibody binding region
P30		/note="computer-predicted antigenic determinant"
P31	Disulfide-bond	136
P32		/note="preserved in immunogenised constructs"
P33	Region	136. 10
P34		/label= insertion region
P35		/note="suitable for foreign T helper epitope insertion"
P36	Region	269. 289
P37		/label= insertion region
P38	Region	328. 324
P39		/note="suitable for foreign T helper epitope insertion"
P40	Region	328. 324
P41		/label= antibody binding region
P42		/note="computer-predicted antigenic determinant"
P43	Region	442. 465
P44		/label= insertion region
P45		/note="suitable for foreign T helper epitope insertion"
P46	Disulfide-bond	466

PT	Region	/note="preserved in immunogenetic constructs"
PT	Region	/label="antibody-binding-region
PT	Region	/note="computer-predicted antigenic determinant"
PT	Region	482..487
PT	Region	/note="antibody-binding-region
PT	Region	/note="experimentally found B cell epitope"
PT	Region	488..514
PT	Region	/label="insertion-region
PT	Disulfide bond	/note="suitable for foreign T helper epitope insertion"
PT	Disulfide bond	598..630
PT	Region	/label="insertion-region
PT	Region	/note="suitable for foreign T helper epitope insertion"
PT	Region	603..663
PT	Region	/label="insertion-region
PT	Region	/note="suitable for foreign T helper epitope insertion"
PT	Region	672..699
PT	Region	/label="insertion-region
PT	Region	/note="suitable for foreign T helper epitope insertion"
PT	Region	711..719
PT	Region	/label="epitope
PT	Region	716..723
PT	Region	/note="antibody-binding-region
PT	Region	/label="experimentally found B cell epitope and computer-predicted antigenic determinant"
PN	MO200020027-A2.	
XX	13-APR-2000.	
XX	05-OCT-1999;	99MO-DK00525.
XX	05-OCT-1998;	98DK-0001261.
XX	05-OCT-1996;	9805-0005011.
XX	DR	N-PSDB: A09454.
XX	(HEB-) M & E BIOTECH AS.	
XX	Steinma L, Mouritzen S, Nielsen KG, Haaning J, Leach D, Dalum I;	
XX	carstam A, Blix P, Karlsson G.	
XX	WPI: 2000-34917/30.	
XX	DR	N-PSDB: A09454.
XX	including immune responses to weakly immunogenic, tumor-associated	
XX	peptide antigens for the treatment of breast and prostatic cancer	
PS	Claim 56: Page 184-187: 220P: English.	

AC	CC	Y92643;
AD	CD	10-AUG-2000 (first entry)
AE	DE	Mutant human prostate specific membrane antigen construct, hpsm1.0.
AF	EN	Prostate specific membrane antigen; immunogenized construct; mutant.
AG	FR	Prostate specific membrane antigen; immunogenized construct; mutant.
AH	FM	Prostate cancer; cell-associated peptide antigen, foreign epitope.
AI	OS	synthetic.
AL	XX	
AM	XX	
AN	XX	
AO	XX	
AP	XX	
AQ	XX	
AR	XX	
AS	XX	
AT	XX	
AV	XX	
AW	XX	
AX	XX	
AY	XX	
AZ	XX	
BA	XX	
BB	XX	
BC	XX	
BD	XX	
BE	XX	
BF	XX	
BG	XX	
BH	XX	
BI	XX	
BJ	XX	
BK	XX	
BL	XX	
BM	XX	
BN	XX	
BO	XX	
BP	XX	
BQ	XX	
BR	XX	
BS	XX	
BT	XX	
BV	XX	
BW	XX	
BX	XX	
BY	XX	
BZ	XX	
CA	XX	
CB	XX	
CC	XX	
CD	XX	
CE	XX	
CF	XX	
CG	XX	
CH	XX	
CI	XX	
CJ	XX	
CK	XX	
CL	XX	
CM	XX	
CN	XX	
CO	XX	
CP	XX	
CQ	XX	
CR	XX	
CS	XX	
CT	XX	
CU	XX	
CV	XX	
CW	XX	
CX	XX	
CY	XX	
CA	XX	
CB	XX	
CC	XX	
CD	XX	
CE	XX	
CF	XX	
CG	XX	
CH	XX	
CI	XX	
CJ	XX	
CK	XX	
CL	XX	
CM	XX	
CN	XX	
CO	XX	
CP	XX	
CQ	XX	
CR	XX	
CS	XX	
CT	XX	
CU	XX	
CV	XX	
CW	XX	
CX	XX	
CY	XX	
CA	XX	
CB	XX	
CC	XX	
CD	XX	
CE	XX	
CF	XX	
CG	XX	
CH	XX	
CI	XX	
CJ	XX	
CK	XX	
CL	XX	
CM	XX	
CN	XX	
CO	XX	
CP	XX	
CQ	XX	
CR	XX	
CS	XX	
CT	XX	
CU	XX	
CV	XX	
CW	XX	
CX	XX	
CY	XX	
CA	XX	
CB	XX	
CC	XX	
CD	XX	
CE	XX	
CF	XX	
CG	XX	
CH	XX	
CI	XX	
CJ	XX	
CK	XX	
CL	XX	
CM	XX	
CN	XX	
CO	XX	
CP	XX	
CQ	XX	
CR	XX	
CS	XX	
CT	XX	
CU	XX	
CV	XX	
CW	XX	
CX	XX	
CY	XX	
CA	XX	
CB	XX	
CC	XX	
CD	XX	
CE	XX	
CF	XX	
CG	XX	
CH	XX	
CI	XX	
CJ	XX	
CK	XX	
CL	XX	
CM	XX	
CN	XX	
CO	XX	
CP	XX	
CQ	XX	
CR	XX	
CS	XX	
CT	XX	
CU	XX	
CV	XX	
CW	XX	
CX	XX	
CY	XX	
CA	XX	
CB	XX	
CC	XX	
CD	XX	
CE	XX	
CF	XX	
CG	XX	
CH	XX	
CI	XX	
CJ	XX	
CK	XX	
CL	XX	
CM	XX	
CN	XX	
CO	XX	
CP	XX	
CQ	XX	
CR	XX	
CS	XX	
CT	XX	

[illegible]

XX	MM	prostate cancer; cell-associated peptide antigen; foreign epitope
CO	XX	Homo sapiens.
PI	Key	Location/Qualifiers
PI	Region	30..51
PT		/label= "insertion_region"
PT		/note= "suitable for foreign T helper epitope ins"
FT	Region	153..173
FT		/label= "insertion_region"
PT		/note= "suitable for foreign T helper epitope ins"
FT	Region	206c23..219
FT		/label= "insertion_region"
PT		/note= "suitable for foreign T helper epitope ins"
FT	Region	241..267
FT		/label= "insertion_region"
PT		/note= "suitable for foreign T helper epitope ins"
FT	Region	385..408
FT		/label= "insertion_region"
PT		/note= "suitable for foreign T helper epitope ins"
FT	Region	406c45..427
FT		/label= "insertion_region"
PT		/note= "suitable for foreign T helper epitope ins"
FT	Region	541..573
FT		/label= "insertion_region"
PT		/note= "suitable for foreign T helper epitope ins"
FT	Region	586..605
FT		/label= "insertion_region"
PT		/note= "suitable for foreign T helper epitope ins"
FT	Region	595c42..612
FT		/label= "insertion_region"
PT		/note= "suitable for foreign T helper epitope ins"
XX	XX	W0300020027.N2.
XX	XX	13-APR-2000.
XX	XX	05-OCT-1999; 99NO-DK00525.
XX	XX	05-OCT-1998; 98DK-0010261.
PR	20-OCT-1998; 98DS-0050111.	
XX	(MEMT) M & E BIOTECH AS.	
XX	Steinae L., Moultehen S., Nielsen KG., Haaning J., Leach D., Dalnu	
PI	Gautam A., Blrk P., Karlsson G.	
DN	WFI: 2000-349917/30.	
DB	N-PDOB: A09454.	
XX	XX	Inducing immune responses to weakly immunogenic, tumor associated

XX	prostate cancer; cell-associated peptide antigen; foreign epitope.
XX	Homo sapiens.
XX	
PI	Key
PI	Region
PF	Location/Qualifiers
PF	30..51
PF	/label=insertion_region
PF	/note=*suitable for foreign T helper epitope insertion
PF	133..173
PF	Region
PF	/label=insertion_region
PF	/note=suitable for foreign T helper epitope insertion
PF	72..96
PF	/label=insertion_region
PF	/note=*suitable for foreign T helper epitope insertion
PF	341..267
PF	Region
PF	/label=insertion_region
PF	/note=*suitable for foreign T helper epitope insertion
PF	385..408
PF	Region
PF	/label=insertion_region
PF	/note=suitable for foreign T helper epitope insertion
PF	406..457
PF	Region
PF	/label=insertion_region
PF	/note=*suitable for foreign T helper epitope insertion
PF	541..573
PF	Region
PF	/label=insertion_region
PF	/note=*suitable for foreign T helper epitope insertion
PF	586..605
PF	Region
PF	/label=insertion_region
PF	/note=*suitable for foreign T helper epitope insertion
PF	593..612
PF	Region
PF	/label=insertion_region
PF	/note=*suitable for foreign T helper epitope insertion
XX	WO200020027 A2.
XX	
PD	13-APR-2000.
PF	
PF	05-OCT-1999;
PF	99MO-DK00525.
PF	
PF	05-OCT-1998;
PF	98DK-0001261.
PR	20-OCT-1998;
XX	98DC-0005011.
XX	
XX	(MEME-) M & E BIOTECHE AS.
XX	
PI	Steinhilber J, Moutlezen S, Nielsen KG, Heaning J, Leach D, Dalum I;
PI	Gautam A, Birk P, Kristensen G;
DR	MPI: 2000-349917/30.
DR	N-P50B: A09454.
XX	
XX	Inducing immune responses to weakly immunogenic, tumor associated

PA
X5 Example 1; Page : 7; 220pb; English.

XX
XX
XX
XX This is a splice variant of human prostate specific membrane antigen
XX
XX CC claimed method as an antineoplastic to induce a CTL response. Subdomain
XX CC CTL epitopes, antibody binding regions and a CTL residues involved
XX CC disulfide bonds are preserved in the immunogenetic forms. Regions
XX CC suitable for the insertion of foreign T helper epitopes were identified.
XX CC immunogenic cell-associated peptide antigens (PA) such as those
XX CC associated with cancers (i.e. self-proteins), for example, human
XX CC prostate specific membrane antigen (PSM), heretofold (2 Herz) and/or
XX CC fibronectin growth factor bb (FGFB). The method comprises effecting
XX CC the expression of a nucleic acid sequence encoding a protein or polypeptide
XX CC animal immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte)
XX CC group derived from the PA and/or at least 1 B-cell group derived from
XX CC cell-associated PAs and (2) at least 1 first T helper cell group which
XX CC humoral/mucosal response comprising a substantial part of all known and
XX CC predicted CTL and B-cell epitopes of the respective PA and including
XX CC at least one foreign T helper epitope are also claimed. The method is u
XX CC to treat prostate, prostate/breast or breast cancer when the PA is hu
XX CC PSM, FGFB and Herz, respectively.

XX
XX Sequence 693 AA:

XX
XX
XX

Dnury Match 98.2%; Score 693; Db 21; Length 693;
Beat Local Similarity 100.0%; Pred. No. of Gaps
Matched 693; Conservative 0; Mismatched 0; Indels 0; Gaps
0

OY 14 MKAPDLEKATNRYENRQIDPAGKQNTOLAKGSGVGRGKQIAADYLITL 60
Db 1 maffldklskkhktlmyfbphlgrenqqlaqdqgkegladwvshndydl 60

OY 74 SYFNTHPIPTISINEDGNIPWLSDEPPCTENSDIVTPSRAFSPOCKSCGLAVY 133
Db 6 fynkthpiptislnedgnipwlsdeppctenstdivtpspasfspoockscglav 133

OY 134 MWAEDEPFKEHDKNIKGGCVGIARCGGVGRKKRNKAQAACGYLDSDAFAFPA 190
Db 121 mwaeedepfkednkikggcvgiarcggvgrkkrnkaqaacgyldsdafafpa 190

OY 194 GVASDPDMNIDSGVGKGAJLNINACADYRTQCPANVAIRNIAEKVGSFVHPFR 253
Db 181 gvassdpdmnidsgvgkgaajlninacadyrtqcpanvaairniaekvgsfvhpfr 253

OY 254 CYVDAGQLLEKMGSAFPDSRSROSILNPVFQCFNGFTQYAKIKHIIHSNRIVTIV 313
Db 240 cyvdagqllekmgsafpdsrsrosilnpvfqcfngftqyakikhiihsnrivtiv 313

[illegible][illegible]


```
Query Match 91.1%; Score 643; DB 21; Length 750;
Beat Local Similarity 100.0%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 VELAHYVTLSTNPKHTPTSTINENKMTSIFPPPCYENSGDTPPSPASRQ 123
DB 108 velahyvtlshpntkhtptstlnenkmstsfpppcyengsdtpspasrq 167
OY 124 GPEODLYVYFAEDPPTLKPMKINGCIVYACGVKQNTYKNAQAKVYL 183
DB 168 gpeodlyvyfaedpptlkpmkingcivyacgvkqntyknanaqvyl 227
OY 184 YSDPAVYKQVSPKQKDCGQKQKILNKAGDPLTQGVYANETAKETAEV 243
DB 228 ysdpavykqvspkqkdcgqkqkilkagdpdltqgvyanetaketae 287
OY 244 GUSGTPVPTCTTQAGLLEKMGSAFPPSSKQSLKPPVNGKPGKSTYQVNH 303
DB 288 gusgtpvptcttqagllekmgsafppsskqslkppvngkpgkstyq 347
OY 304 STNTEYKINVTGTLKGAVERVYILGCHDSVFGSDIPDQSAVYHETVSGT 363
DB 348 stnteysinvtgtlkgavervyilgchdsvfgsdipdqsavyhett 407
OY 364 SCWRPRTPLASNDAREFGLSGSTFMAEENSRILDERGAYINDSIEKNT 423
DB 408 scwrprtpllasndarefglsgstfmaeenrslldergayindsiek 467
OY 424 PLATSLVHLTKELSPDQKSKLSYMTKAPPPSPGSKSLSGKQNPFPOR 483
DB 468 platslvhltkelspdqkkslymtkappspgskslsgkqnpfpor 527
OY 484 LGIAGCAATKMTKMTKFGVGYHAYVETELVETFDPPRYHLYAVGQVPEL 543
DB 528 lgiagcaatkmmtkmtkfgvgyhayvetelvetfdppryhlyavgv 587
OY 544 ANSTYRQCDYAVYATYAKTYSIGMHQDQMTYCVSDGKSTANVYETLS 603
DB 588 anstyrqcdyavyatyaktysigmhqdmtycvsdgkstanyvetls 647
OY 604 BRADPYSANVYLRNNDQGLTLEATDPLGPPFPRHRYTVASSHNKAGES 663
DB 648 bradpysanvylrnndqgltleatdplgppfprhrytvasshngag 707
OY 664 YVAFLEISVDPVPAKMGVKNQIVYAAFPYQAAETLSFVA 706
DB 708 yvafleisvdpvpakmgvknqivyaafpyqaaetlsfva 750

RESULT 14
```

```
CC Immune responses against weakly immunogenic cell-associated peptide
CC antigen (PA) such as those associated with cancer (self-protein), e.g.
CC human prostate specific membrane antigen (PSM), Her2/gln 2 (Her2) and/or
CC fibroblast growth factor 8b (FGF8b). The method comprises effecting
CC antibody growth factor by antigen producing cells (APCs) of the
CC animal immune system (AIS) to generate a 1 B-cell group (1B-cell)
CC cell-derived from the PA and/or at least 1 B-cell group derived from the
CC cell-associated PA; and (2) at least 1 first T helper cell group which is
CC foreign to the animal. Analogues of human PSM, human Her2 and
CC predicted CTL and B-cell epitopes of the respective PA and/or
CC at least one foreign T helper epitope are also claimed. The method is
CC used to treat prostate, prostate/breast or breast cancer when the PA is human
CC Note: This sequence was derived from the wild type human PSM
CC (Y92619), which appears on pages 184-187 of the specification.
XX
XX Sequence 750 AA:

Query Match 89.1%; Score 629; DB 21; Length 750;
Beat Local Similarity 100.0%; Pred. No. 0;
Matches 629; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSENKATIPFNKKAFLDLELANIKFLYETFOPLHAGTQNPQALQIOSKHT 60
DB 45 sseknatipfnkkafldelelanikflyetfoplhagtqnpqalqiosk 104
OY 61 LAGSELAHYVTLSTNPKHTPTSTINENKMTSIFPPPCYENSGDTPPSPAS 120
DB 105 lagselahyvtlshpntkhtptstlnenkmstsfpppcyengsdtpsp 164
OY 121 GPEODLYVYFAEDPPTLKPMKINGCIVYACGVKQNTYKNAQAKVYL 180
DB 165 gpeodlyvyfaedpptlkpmkingcivyacgvkqntyknanaqvyl 224
OY 181 YSDPAVYKQVSPKQKDCGQKQKILNKAGDPLTQGVYANETAKETAEV 240
DB 225 ysdpavykqvspkqkdcgqkqkilkagdpdltqgvyanetaketae 284
OY 241 EAVGSPJPWPICGTDAQGLLEKMGSAFPPSSKQSLKPPVNGKPGKSTYQV 300
DB 285 eavgspjwpicgtdaqglllekmgsafppsskqslkppvngkpgkstyq 344
OY 301 HHSNTGYATRYVYIGTLGAVEDRVYILGCHDSVFGSDIPDQSAVYHETV 360
DB 345 hhsntgyatryvyigtlgavedrvyilgchdsvfgsdipdqsavyhett 404
OY 361 LKRGQNPRTPLASNDAREFGLSGSTFMAEENSRILDERGAYINDSIEKNT 420
DB 405 lkrgqnprrtllasndarefglsgstfmaeenrslldergayindsiek 464
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```
Y92630
XX 1-20 Y92630 standard. Protein: 750 AA.
XX AC Y92630:
XX
XX 10-AUG-2000 (first entry)
XX
XX Mutant human prostate specific membrane antigen construct, hpsm10.1.
XX
XX Prostate specific membrane antigen; immunogenized construct; mutant;
XX prostate cancer; cell-associated peptide antigen; foreign epitope.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 21..41
XX /label= p30
XX /note= foreign epitope*
XX
XX Peptide 674..688
XX /label= p2
XX /note= foreign epitope*
XX
XX MO200020027-A2.
XX
XX 13-APR-2000.
XX
XX 05-OCT-1999. 9980-DR00525.
XX
XX 05-OCT-1998. 98DK-0001261.
XX
XX 20-OCT-1998. 98DS-0105011.
XX
XX (HEBI-) M & B BIOTECH AS.
XX
XX Steinha L, Mouritsen S, Nielsen KC, Haaning J, Leach D, Dalum I;
XX Gautam A, Birk P, Karlsson G;
XX WPI: 2000-349317/30.
XX
XX Inducing immune responses to weakly immunogenic, tumor associated
XX peptide antigens for the treatment of breast and prostate cancer
XX
XX Example 1. Page 1: 220pp; English.
XX
XX Y92637-49 are mutant immunogenized human prostate specific membrane
XX antigen (PSM) constructs, which contain foreign epitopes (p2 and/or p30).
XX The immunogenic analogues of PSM can be used in the claimed method as an
XX adjuvant for immunization of subjects. The analogues of PSM can be used
XX binding regions and cysteine residues involved in disulfide bonds are
XX preserved in the immunogenized forms. The method is used for inducing
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OY 421 GCPYATYSVYNT/ATEZKSPDQKSGYVYHAYVETELVETFDPPRYHLYAVGQV 480
DB 465 gcpyatysvnt/atelkspdqskgyvyhayevelvetfdppryhlyavgqv 524
OY 481 FQGLTISGKATKMTKMTKFGVGYHAYVETELVETFDPPRYHLYAVGQV 540
DB 525 fqgltskattkmmtkmtkfgvgyhayvetelvetfdppryhlyavgqv 584
OY 541 PRLANSTVLPDQDQVAVYATYAKTYSIGMHQDQMTYCVSDGKSTANVYETLS 600
DB 585 prlanstvlpdqdqvavyatyaktysigmhqdmtycvsdgkstanyvetls 644
OY 601 RFERLQDQDPSRPYVLRNNDQGLTLEATDPLGPPFPRHRYTVASSHNKAGES 663
DB 645 rferrldqdqpsrpyvlrnndqgltleatdplgppfprhrytvasshngag 707

RESULT 15
XX
XX Y92641 standard. Protein: 750 AA.
XX AC Y92641:
XX
XX 10-AUG-2000 (first entry)
XX
XX Mutant human prostate specific membrane antigen construct, hpsm10.0.
XX
XX Prostate specific membrane antigen; immunogenized construct; mutant;
XX prostate cancer; cell-associated peptide antigen; foreign epitope.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 674..688
XX /label= p2
XX /note= foreign epitope*
XX
XX MO200020027-A2.
XX
XX 13-APR-2000.
XX
XX 05-OCT-1999. 9980-DR00525.
XX
XX 05-OCT-1998. 98DK-0001261.
XX
XX 20-OCT-1998. 98DS-0105011.
XX
XX (HEBI-) M & B BIOTECH AS.
XX
```

P1 Steinae L., Mouritsen S., Nielsen KG., Haaning J., Leach D., Dalum I.;
 P2 Gautam A., Birk P., Karlsson G.;
 WPI: 2000-349317/30.
 Inducing immune responses to weakly immunogenic, tumor associated
 peptide antigens for the treatment of breast and prostate cancer
 Example 1: Page 1: 220pp: English.
 CC Y92427-49 are mutant immunogenized human prostate specific membrane
 CC antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30).
 CC The PSM constructs are immunized into mice. The immunized mice are
 CC antiserum to induce a CTL response. Subdominant CTL epitopes, antibody
 CC binding regions and cysteine residues involved in disulfide bonds are
 CC preserved in the immunogenized forms. The method is used for inducing
 CC immune responses against weakly immunogenic cell-associated peptide
 CC human prostate specific membrane antigen (PSM). Heregulin 2 (Her2) and/or
 CC fibroblast growth factor 8b (FGF8b). The method comprises effecting
 CC simultaneous presentation by antigen producing cells (APCs) of the
 CC animal immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte)
 CC cell-associated P2; and (2) at least 1 first T helper cell group which is
 CC human/murine FGF8b comprising a substantial part of all known and
 CC predicted human/murine FGF8b epitopes. The method is used for inducing AT
 CC to treat prostate, prostate/breast or breast cancer when the P2 is human
 CC PSM, FGF8b and Her2, respectively.
 CC Note: This sequence was constructed from the wild type human PSM
 CC (Y92431), which appears on pages 164-167 of the specification.
 XX Sequence 750 AA:

Query Match 89.1%; Score 629; DB 21; Length 750;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 629; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SENEATNTPHNKAKFLDELAENIKKFLNFPOLPHLAGFONPOLAKOLOSQKERS 60
 DB 45 seneatniphmkafldelakenkikflntqplhlagfongqlakqgqvkets 104
 QY 61 LDGVATNTPHNKAKFLDELAENIKKFLNFPOLPHLAGFONPOLAKOLOSQKERS 120
 DB 105 ldavetahvntqplhlagfongqlakqgqvkets 164
 QY 121 SPOQMBSDIYVYVARTEDPFLKDMKINSGKIVARICAKYKRNQAKLAKG 180
 DB 165 spqmbgdlyvvyartedfllkdmkinksgkivaryvrlcgnkqhknqaglsag 224

PH Key Location/Qualifiers
 PT Peptide 24-38
 PT /label- p2
 PT /label- foreign epitope*
 PT 672-693
 PT /label- P30
 PT /note= "foreign epitope"
 XX WO200020027-A2.
 XX 13-APR-2000.
 XX 05-OCT-1999: 99NO-DE00525.
 XX 05-OCT-1998: 98DK-0001261.
 XX 20-OCT-1998: 98US-0105011.
 XX (HMB-1) M & B BIOTECH AS.
 XX Steinae L., Mouritsen S., Nielsen KG., Haaning J., Leach D., Dalum I.;
 XX Gautam A., Birk P., Karlsson G.;
 XX WPI: 2000-349317/30.
 PT Inducing immune responses to weakly immunogenic, tumor associated
 PT peptide antigens for the treatment of breast and prostate cancer
 XX Example 1: Page 1: 220pp: English.
 CC Y92427-49 are mutant immunogenized human prostate specific membrane
 CC antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30).
 CC The PSM constructs are immunized into mice. The immunized mice are
 CC antiserum to induce a CTL response. Subdominant CTL epitopes, antibody
 CC binding regions and cysteine residues involved in disulfide bonds are
 CC preserved in the immunogenized forms. The method is used for inducing
 CC immune responses against weakly immunogenic cell-associated peptide
 CC human prostate specific membrane antigen (PSM). Heregulin 2 (Her2) and/or
 CC fibroblast growth factor 8b (FGF8b). The method comprises effecting
 CC simultaneous presentation by antigen producing cells (APCs) of the
 CC animal immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte)
 CC cell-associated P2; and (2) at least 1 first T helper cell group which is
 CC human/murine FGF8b comprising a substantial part of all known and
 CC predicted human/murine FGF8b epitopes. The method is used for inducing AT
 CC to treat prostate, prostate/breast or breast cancer when the P2 is human
 CC PSM, FGF8b and Her2, respectively.
 CC Note: This sequence was constructed from the wild type human PSM
 CC (Y92431), which appears on pages 164-167 of the specification.

QY 181 VTIYSDPADTAPQVSPKQKIDPGQGVONKILMLKAGADPLFPGYPAWNAIRKIA 240
 DB 225 vtiysdpadtyfapqvkqkldpgqgvonkllmlkagadplfpgypawnavyrsia 284
 QY 241 EAVGLPSIPVPIGCTYDAOKLERKGSAPDSSNRGSLKAVYVWGPFGFNSFQVKN 300
 DB 265 eavglpsipvpigctydaoklerkgsapdssnrgslkavyvwgpfngfnsfqvkn 344
 QY 301 HINSTNEVTRIVYIGTLNCAVBPDRVYLGCHBSHWFGIDPQGAAYHIEVYRSPT 360
 DB 345 hlnstnevtrivynvlgclncaavbpdrvyylgchbswhvfgidpqgaayhievyrsp 404
 QY 361 LKFGKRRPRRTILFASMDAEPFLGSGTMAEENSLQDRCGVYTNADSGTIDQNTLY 420
 DB 405 lkfgkrprprtllfasmdaepflgsgtmaeenlslqdrconvtnadsgtidqntly 464
 QY 421 DCPYLDVSLVHNLTKELSGPDPGKSLVSEWTKSPGSPGSRISLQSGNDPFG 480
 DB 465 dcpyldevslvhnltkelsgdpdgkslvsewtkspgspgsrslsqsgndpfg 524
 QY 481 RORGLIASGAAVYVWVWVNSGCVPLVSVYVYVYVYVYVYVYVYVYVYVYV 540
 DB 525 rorgliasgaavvwwvwnsgcvplvsvyvyvyvyvyvyvyvyvyvyvyvyvy 584
 QY 541 PEANSLVLPFGCDVAVYVNLKADKITSKNIHQVDEKTCGSEPSLSANVETIAS 600
 DB 585 peanslvlpfgcdvavyvnlkadkitsknihqvdekctcgsepslsanvetias 644
 QY 601 KFSBRLOPDKNSVIVLHNNQDLAFER 628
 DB 645 kfbrlopdksnvivlhnnqdlaferr 673

RESULT 16
 ID: Y92633 standard; Protein: 750 AA.
 XX AC Y92633;
 XX 10-NOV-2000 (first entry)
 DE Mutant human prostate specific membrane antigen construct, hPSM. 10.
 XX Prostate specific membrane antigen; immunogenized construct; mutant;
 XX vaccination; cytotoxic T-lymphocyte; immunity; breast cancer;
 KW prostate cancer; cell-associated peptide antigen; foreign epitope.
 XX Homo sapiens.
 XX Synthetic.
 XX

XX Sequence 750 AA:
 Query Match 89.0%; Score 628; DB 21; Length 750;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 628; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SENEATNTPHNKAKFLDELAENIKKFLNFPOLPHLAGFONPOLAKOLOSQKERS 60
 DB 45 seneatniphmkafldelakenkikflntqplhlagfongqlakqgqvkets 104
 QY 61 LDGVATNTPHNKAKFLDELAENIKKFLNFPOLPHLAGFONPOLAKOLOSQKERS 120
 DB 105 ldavetahvntqplhlagfongqlakqgqvkets 164
 QY 121 SPOQMBSDIYVYVARTEDPFLKDMKINSGKIVARICAKYKRNQAKLAKG 180
 DB 165 spqmbgdlyvvyartedfllkdmkinksgkivaryvrlcgnkqhknqaglsag 224
 QY 181 VTIYSDPADTAPQVSPKQKIDPGQGVONKILMLKAGADPLFPGYPAWNAIRKIA 240
 DB 225 vtiysdpadtyfapqvkqkldpgqgvonkllmlkagadplfpgypawnavyrsia 284
 QY 241 EAVGLPSIPVPIGCTYDAOKLERKGSAPDSSNRGSLKAVYVWGPFGFNSFQVKN 300
 DB 265 eavglpsipvpigctydaoklerkgsapdssnrgslkavyvwgpfngfnsfqvkn 344
 QY 301 HINSTNEVTRIVYIGTLNCAVBPDRVYLGCHBSHWFGIDPQGAAYHIEVYRSPT 360
 DB 345 hlnstnevtrivynvlgclncaavbpdrvyylgchbswhvfgidpqgaayhievyrsp 404
 QY 361 LKFGKRRPRRTILFASMDAEPFLGSGTMAEENSLQDRCGVYTNADSGTIDQNTLY 420
 DB 405 lkfgkrprprtllfasmdaepflgsgtmaeenlslqdrconvtnadsgtidqntly 464
 QY 421 DCPYLDVSLVHNLTKELSGPDPGKSLVSEWTKSPGSPGSRISLQSGNDPFG 480
 DB 465 dcpyldevslvhnltkelsgdpdgkslvsewtkspgspgsrslsqsgndpfg 524
 QY 481 RORGLIASGAAVYVWVWVNSGCVPLVSVYVYVYVYVYVYVYVYVYVYVYV 540
 DB 525 rorgliasgaavvwwvwnsgcvplvsvyvyvyvyvyvyvyvyvyvyvyvyvy 584
 QY 541 PEANSLVLPFGCDVAVYVNLKADKITSKNIHQVDEKTCGSEPSLSANVETIAS 600
 DB 585 peanslvlpfgcdvavyvnlkadkitsknihqvdekctcgsepslsanvetias 644
 QY 601 KFSBRLOPDKNSVIVLHNNQDLAFER 628
 DB 645 kfbrlopdksnvivlhnnqdlaferr 673

[illegible]

	CC	antivaccine to induce a CTL response. Subdominant CTL epitopes, antibody
96	CC	binding regions and cysteine residues involved in disulfide bonds are
97	CC	immune responses against weakly immunogenic cell-associated peptide
98	CC	antigens (Pa) such as those associated with cancers (cell proteins), e.g.
99	CC	human prostate specific membrane antigen (PSM), Herpesin 2 (Her2) and/or
100	CC	herpesvirus presentation by CD80+ dendritic method complexes eliciting
101	CC	antitumor immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte)
102	CC	group derived from the PA and/or; at least 1 B-cell group derived from the
103	CC	cells associated Pa; and (2) at least 1 first T helper cell group which is
104	CC	human/murine FcγR comprising a substantial part of all known and
105	CC	predicted CTL and B-cell epitopes of the respective PA and including at
106	CC	least one foreign T helper epitope are also claimed. The method is used
107	CC	to predict, produce, proliferate/breast or breast cancer when the PA is human
108	CC	Note: This sequence was constructed from the wild type human PSM
109	XX	(Y92A19), which appears on pages 184-187 of the specification.
110	XX	Sequence 750 AA:
111	Query Match	79.6%; Score 562; Db 21; Length 750;
112	Best Local Similarity	100.0%; Pied No; 0;
113	Matches 362;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
114	QY	1 SNNANVTNTHNAKVEPEELAKENIKFLANETDPIHAGTEONLQAIGOSGNEFRS 60
115	Db	45 ssnanvshphmalmldklskeklxkvltvdhphlsgtemqqlaaqqgqqeqky 104
116	QY	61 LDSEELAVLVLSVPPNRNTIISINDGNFPTSLSPPEPZYENSIVTPSSPAF 120
117	Db	105 ldsaelavlvlsppnrntiisindgnfptslsppepzyensivtpsspafl 164
118	QY	121 SPQNGEEDLVYVVAATDEFPPLTFRMRNTNSGRTITAAQKGVKYNALAGAE 180
119	Db	165 spqngeddlvyvvatdelfrmtlmibncsgvlalavryyfgnkrkhdlaagys 224
120	QY	181 VTIISPADATACSGESFGDNDCGGCGOCHILKKAKGCDITTCIPAMETARICGA 240
121	Db	225 vtiispadatacsgefsfgdnccggcgchilkkakgcdittpametaricga 284
122	QY	241 EAVGLPSIPVPGTGIDYDTALKKGASAPPDSSWRKSIAVYVDFVDFGPFQSDPY 300
123	Db	285 eavglpshivpgtgidydtalkkgasapddswnksiaavydvdfvgpfqsdpy 344
124	QY	301 HHTHEMTNNTVVGTLGAVGPBPRVYLDSGRDSWVSG IDMSGCAAVMEIVNSPCT 360
125	Db	345 hhthemtnntvvgtlgavgpbrvyldsgrdswwsvgs idmsgcaavmeivnsprt 404

QY	361	LTKEGMPRRRTLLFASMDKEEPFGSLGSLTMAEHSRLGLGRCVAYINADSIQGHVTLV	420
QY	405	LTKEGMPRRRTLLFASMDKEEPFGSLGSLTMAEHSRLGLGRCVAYINADSIQGHVTLV	464
Db		LTKEGMPRRRTLLFASMDKEEPFGSLGSLTMAEHSRLGLGRCVAYINADSIQGHVTLV	464
QY	421	DCPTPLKSVSYVNIITRELKSPDRPEKGLVESHMTKSPSPSPGSDRIENLGGSDPEVP	480
Db	465	dcptplksvsyvniitrelkspdrpekglveshmtkspspspgspdrienglsgndevf	524
QY	481	PGSLISGLSARARTANETPNKSPGSLVSHYETVELVEVPIDPMFRLTLTAQRCGV	540
Db	524	pgslisglsarartanetpnrkspgslvshyetyelvelvevpidpmfrltltvaqvrgsw	584
QY	541	PELANSVPIPCDGRVAYVLRK 562	
Db	585	pelansvipcdgrvayvlrk 606	
RESULT	18		
Y92629			
Y92629		standard. Protein: 750 AA.	
Y92629			
AC	Y92629		
XX			
XX	10-M05-2000	(first entry)	
XX			
DB		Mutant human prostate specific membrane antigen construct, hps98.1.	
XX			
XX		Prostate specific membrane antigen; immunogenized construct; mutant;	
XX		vesiculation; cytoxic T-lymphocyte immunity; breast cancer;	
XX		prostate cancer; cell-associated peptide antigen; foreign epitope.	
OS	Homo sapiens.		
XX			
XX		Synthetic.	
XX			
XX	Key	Location/Qualifiers	
XX	Peptide	21..41	
XX		/label= f30	
XX	Peptide	/note= foreign epitope*	
XX		/label= f20	
XX		/label= p2	
XX		/note= "foreign epitope"	
XX	W0200020037-R2.		
XX			
XX	13-APR-2000.		
XX			
XX	05-OCT-1999.	99M0-DR00525.	
XX			
XX	05-OCT-1998.	98DR-0001561.	
XX	20-OCT-1998.	98US-0105011.	

[illegible]

[illegible]

Query Match 61.0%; Score 431; DB 21; Length 750

Mon Apr 7 11:14:10 2001

us-08-031-803-2.ccopy_45_750_oilgr.xag

OS	Synthetic.
FH	Key
FH	Peptide
FT	/Abeta1/P2
FT	301...321
FT	/Abeta1_P30
FT	/note="foreign epitope"
FN	MO20002002742.
PD	13-APR-2000.
PE	05-OCT-1999; 59NC-DK00525.
PR	05-OCT-1998; 96DR-0001261.
XX	20-OCT-1998; 96DS-0105011.
PA	(MEDI-) M & E BIOCHEM AS.
P1	Steinla U., Mouritzen S., Nielsen KG., Haaning J., Leach D., Dalum I.,
P2	Gustavsen A., Birk P., Natanson G.
DR	WPI; 2000-34931730.
P7	Inducing immune responses to highly immunogenic, tumor associated
XX	peptide antigens for the treatment of breast and prostatic cancer
PS	Example 1; Page 7; 22ppr; English.
CC	Y19Z627-4 are mutant immunoprecipitated human prostate specific membrane
CC	antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30
CC	The immunogenic analogues of PSM can be used in the claimed method as an
CC	adjuvant to induce a CTL response. Subdominant CTL epitopes, antibodies
CC	binding vaccine to induce a CTL response. The method is used for inducing
CC	immune responses against weakly immunogenic cell-associated peptide
CC	antigens (PA), such as those associated with cancers (self-proteins) and/or
CC	ribosomal growth factor Ab (PGSb). The method includes a step of
CC	animal immune presentation by antigen producing cells (APCs) of the
CC	animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte)
CC	cell-associated PA, and (2) at least 1 B-cell group derived from which
CC	foreign to the animal. Analogues of human PSM, human Her2 and
CC	human/murine PGSP comprising a substantial part of all known and
CC	least one foreign T cell epitopes of the respective PA, and including at
CC	to treat prostate, prostatic/breast or breast cancer when the PA is human
CC	PSM, PGSP and Her2, respectively.

[illegible]

Homo sapiens

Mon Apr 9 11:14:10 2001

us-08-403-803-2_copy_45_750.011g.rag

Page 80

CC note: this sequence was constructed from the wild type human
CC (Y92619), which appears on pages 184-187 of the specification
XX
SQ Sequence 750 AA;

Query Match	60.83	Score 429	DB 21	Length 750
Best Local Similarity	100.0%	Pred. No. 0		
Matches 429; Conservative	0	Mismatches 0	Indels 0	Gaps 0

[illegible]

DR Mutant human prostate specific membrane antigen construct, hPSM6.1.
 CC Prostate specific membrane antigen, immunogenized construct; mutant.
 CC Vaccination: cytotoxic T-lymphocyte immunogenized construct; mutant.
 CC Prostate cancer: cell-associated peptide antigen; foreign epitope.
 CC Homo sapiens.
 CC Synthetic.
 CC Key Location/Qualifiers
 FT Peptide 21..41
 FT /label= P20
 FT /note= "foreign epitope"
 FT Peptide 448..463
 FT /label= P2
 FT /note= "foreign epitope"
 CC MO200020027-A2.
 CC 13-APR-2000.
 CC 05-OCT-1999: 99MO-DR00525.
 CC 05-OCT-1998: 98DK-0001261.
 CC 20-OCT-1998: 98DK-0105011.
 CC (MEDI-) M & B BIOTECH AS.
 CC Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;
 CC Gaetum A, Birk P, Karlsson G;
 CC WPI: 2000-346917/30.
 CC Inducing immune responses to weakly immunogenic, tumor associated
 CC peptide antigens for the treatment of breast and prostate cancer
 CC Example 1: Page -1: 220pp: English.
 CC Y92637-49 are mutant immunogenized human prostate specific membrane
 CC antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P20).
 CC The constructs are immunogenized and used to induce a CTL response. Antibody
 CC binding regions and cysteine residues involved in disulfide bonds are
 CC preserved in the immunogenized forms. The method is used for inducing
 CC immune responses against weakly immunogenic cell-associated peptide
 CC antigens (PA) such as those associated with cancer (cell proteins), e.g.
 CC human prostate specific membrane antigen (PSM), heregulin 2 (her2), and/or
 CC fibroblast growth factor 8b (FGF8b). The method comprises effecting
 CC simultaneous presentation by antigen producing cells (APCs) of the
 CC antigen (PA) and a foreign epitope (P2 and/or P20) derived from the
 CC group derived from the PA and/or at least 1 B-cell group derived from the

CC cell-associated PA; and (2) at least 1 first T helper cell group which is
 CC foreign to the animal. Analogues of human PSM, human Her2 and
 CC human FGF8b are used as antigens. The method is used for inducing
 CC predicted CTL and B-cell epitopes of the respective PA and including at
 CC least one foreign T helper epitope are also claimed. The method is used
 CC to treat prostate, prostate/breast or breast cancer when the PA is human
 CC PSM, FGF8b and Her2, respectively.
 CC The method is used for inducing immune responses against weakly
 CC immunogenic cell-associated peptide antigens (PA) such as those
 CC associated with cancer (cell proteins), e.g. human prostate specific
 CC antigen (PSM), heregulin 2 (her2), and/or fibroblast growth factor 8b
 CC (FGF8b), which appears on pages 184-187 of the specification.
 CC XX Sequence 750 AA:
 CC
 CC Query Match 57.18; Score 403; DB 21; Length 750;
 CC Best Local Similarity 100.0%; Pred. No. 0;
 CC Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC 1 SGNBANTPTKHNKAAFDIEKAKYKIFKFLNTPQIPHLAAGTBNQOLANOTGSKERC 60
 CC 45 seneatnlpkhnkafidekkaenlklyntfiphlagteqnglakqgqyqefg 104
 CC 61 LSVELANDVLSPTNKTHTNTISINDGNEPISLFEPPPCGDNVSDVPPPSAF 120
 CC 105 lsvaelandvylspnkhbnpj40lindngnefnscslcgepppgdnvsklpppsaf 164
 CC 121 SPOQNBODLVYVNAKTEDFKLRDNKINCSCATYIARGVKGNKNAQAKNG 180
 CC 165 spqnpbgdlvynvartedfklrckmknscgltvlargvkgnknaqakng 224
 CC 225 vilyedpadyfapvksyqdgynlp99vqgnllhngagadpl99yanevysr 284
 CC 241 EAVGLPSIPVHPGOTYDQKLEKMGSAFPPDSHMGSLAVPWNGPOTGFRNQK 300
 CC 285 eavglpsipvhpqotydqkllerkmgsafppdshmgslavpwngpofgfrnqk 344
 CC 301 HNSTREVTYVNGTLCNKAVERPARYLGGHDSVFGIDPQSAVMEKVSFRT 360
 CC 345 hnstrevtyvngtllcngkaverparylggghdsvfgidpqsavmekvsf 404
 CC 361 LKESGMRRTILFASNDASEPCLGSTPAEENSLQRCV 403
 CC 405 lksgmrtrtllfasndasepclgstpaeeenslqrsv 447
 CC
 CC RESULT 27
 CC Y92631
 CC ID Y92631 standard: Protein: 750 AA.
 CC NC Y92631:

XX 07-AUG-2000 (first entry)
 CC Mutant human prostate specific membrane antigen construct, hPSM1.6.
 CC Prostate specific membrane antigen; immunogenized construct; mutant;
 CC Vaccination: cytotoxic T-lymphocyte immunogenized construct; mutant;
 CC Prostate cancer: cell-associated peptide antigen; foreign epitope.
 CC Homo sapiens.
 CC Synthetic.
 CC Key Location/Qualifiers
 FT Peptide 24..38
 FT /label= P2
 FT /note= "foreign epitope"
 FT Peptide 443..463
 FT /label= P10
 FT /note= "foreign epitope"
 CC MO200020027-A2.
 CC 13-APR-2000.
 CC 05-OCT-1999: 99MO-DR00525.
 CC 05-OCT-1998: 98DK-0001261.
 CC 20-OCT-1998: 98DK-0105011.
 CC (MEDI-) M & B BIOTECH AS.
 CC Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;
 CC Gaetum A, Birk P, Karlsson G;
 CC WPI: 2000-346917/30.
 CC Inducing immune responses to weakly immunogenic, tumor associated
 CC peptide antigens for the treatment of breast and prostate cancer
 CC Example 1: Page -1: 220pp: English.
 CC Y92637-49 are mutant immunogenized human prostate specific membrane
 CC antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P20).
 CC The constructs are immunogenized and used to induce a CTL response. Antibody
 CC binding regions and cysteine residues involved in disulfide bonds are
 CC preserved in the immunogenized forms. The method is used for inducing
 CC immune responses against weakly immunogenic cell-associated peptide
 CC antigens (PA) such as those associated with cancer (cell proteins), e.g.
 CC human prostate specific membrane antigen (PSM), heregulin 2 (her2), and/or
 CC fibroblast growth factor 8b (FGF8b). The method comprises effecting

CC simultaneous presentation by antigen producing cells (APCs) of the
 CC antigen (PA) and a foreign epitope (P2 and/or P20) derived from the
 CC group derived from the PA and/or at least 1 B-cell group which is
 CC foreign to the animal. Analogues of human PSM, human Her2 and
 CC human FGF8b are used as antigens. The method is used for inducing
 CC predicted CTL and B-cell epitopes of the respective PA and including at
 CC least one foreign T helper epitope are also claimed. The method is used
 CC to treat prostate, prostate/breast or breast cancer when the PA is human
 CC PSM, FGF8b and Her2, respectively.
 CC The method is used for inducing immune responses against weakly
 CC immunogenic cell-associated peptide antigens (PA) such as those
 CC associated with cancer (cell proteins), e.g. human prostate specific
 CC antigen (PSM), heregulin 2 (her2), and/or fibroblast growth factor 8b
 CC (FGF8b), which appears on pages 184-187 of the specification.
 CC CC Note: This sequence was constructed from the wild type human PSM
 CC (Y92631), which appears on pages 184-187 of the specification.
 CC 50 Sequence 750 AA:
 CC
 CC Query Match 56.48; Score 398; DB 21; Length 750;
 CC Best Local Similarity 100.0%; Pred. No. 0;
 CC Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC 1 SGNBANTPTKHNKAAFDIEKAKYKIFKFLNTPQIPHLAAGTBNQOLANOTGSKERC 60
 CC 45 seneatnlpkhnkafidekkaenlklyntfiphlagteqnglakqgqyqefg 104
 CC 61 LSVELANDVLSPTNKTHTNTISINDGNEPISLFEPPPCGDNVSDVPPPSAF 120
 CC 105 lsvaelandvylspnkhbnpj40lindngnefnscslcgepppgdnvsklpppsaf 164
 CC 121 SPOQNBODLVYVNAKTEDFKLRDNKINCSCATYIARGVKGNKNAQAKNG 180
 CC 165 spqnpbgdlvynvartedfklrckmknscgltvlargvkgnknaqakng 224
 CC 225 vilyedpadyfapvksyqdgynlp99vqgnllhngagadpl99yanevysr 284
 CC 241 EAVGLPSIPVHPGOTYDQKLEKMGSAFPPDSHMGSLAVPWNGPOTGFRNQK 300
 CC 285 eavglpsipvhpqotydqkllerkmgsafppdshmgslavpwngpofgfrnqk 344
 CC 301 HNSTREVTYVNGTLCNKAVERPARYLGGHDSVFGIDPQSAVMEKVSFRT 360
 CC 345 hnstrevtyvngtllcngkaverparylggghdsvfgidpqsavmekvsf 404
 CC 361 LKESGMRRTILFASNDASEPCLGSTPAEENSLQRCV 403
 CC 405 lksgmrtrtllfasndasepclgstpaeeenslqrsv 447
 CC
 CC RESULT 28
 CC Y92648

DE 10-AUG-2000 (first entry)
 D7 Murine prostate specific membrane antigen splice variant.
 D8
 D9 Prostate specific membrane antigen; splice variant; vaccination;
 PM cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer;
 NM prostate cancer; cell-associated peptide antigen; foreign epitope.
 XX
 OS Mus musculus.
 G6 M020000207-72.
 XX
 PD 13-APR-2000.
 XX
 XX 05-OCT-1999; 99MC-DK00535.
 XX
 XX 05-OCT-1998; 98DE-0001261.
 PR 20-OCT-1998; 98DS-0105011.
 XX
 XX (MEDLINE) M & E JOTECX AS.
 XX
 P1 Steina L., Moritsen S., Nielsen KG., Hanning J., Leach D., Dalum I.;
 GA Gautreaux B., Birn P.
 DR WPI: 2000-34693/730.
 N-PSTID: A09459.
 XX
 XX Including immune responses to weakly immunogenic, tumor associated
 PM peptide antigens for the treatment of breast and prostate cancer
 XX
 PS Example 1: Page 210-213; 320P; English.
 CC The claims detail a method for inducing immune responses against weakly
 CC immunogenic cell-associated peptide antigens (PA) such as those
 CC associated with cancers (i.e. self-proteins). For example, human
 CC prostate specific membrane antigen (PSM), hergulin 2 (Her2) and/or
 CC simultaneously presentation by both primary and secondary dendritic
 CC group derived from the PA and/or at least 1 B-cell group derived from the
 CC cell-associated PA, and (2) at least 1 first T helper cell group which
 CC humin/antine Fc γ b2b competing a substantial part of all known and
 CC predicted CTL and B-cell epitopes of the respective PA and including at
 CC least one foreign T helper epitope are also claimed. The method is used
 CC PSM, Fc γ b2b and Her2, respectively.
 XX Sequence 694 AA:

					5.1%; Score 36; DB 21; Length 694;
B	Query Match				Best Local Similarity 100.0% Pred.No. 1-4e-78;
O	Cysteine 36; Conservative			Mismatches 0; Gaps	
X	39S SLRLQKRVAVYNNMSISGVATVADPTDPLNGLVALT 430 				
D	b39 sllrgcrvyaynnadsstlsgnyltvdcplpyvalt 418				
R	RESULT 33				
V	y91661				
I	i92861 standard; Protein; 698 AA.				
A	c y92861;				
T	10-AUG-2000 (first entry)				
X	Mutant murine psm aplice variant construct, mpsw X.				
X	Prostate specific membrane antigen; aplice variant; mutant; X				
X	pmsw X; prostate cancer; cell-associated peptide antigen; foreign epitope. X				
K	Nha musculus:				
S	Synthetic:				
F	Key Location/Qualifiers				
P	Peptide 197..217				
L	/label= P30				
N	MO200002027-A2.				
D	13-APR-2000.				
P	05-OCT-1999; 99NO-DK00525.				
X	05-OCT-1998; 98DR-0001261.				
P	20-OCT-1998; 98DS-005011.				
X	(HBB)- H & B BIOTECH AS.				
E	Steina L., Nourizadeh S, Nielsen KG, Manning J, Leach D, Dalum I, I				
G	Gustafson A, Blin T, Karlsson C,				
D	WPI; 2000-349317/30.				
R	Including immune responses to widely immunogenic, tumor associated P				
P	peptide antigens for the treatment of breast and prostate cancer				

PS Example 1; Page -; 220pp; English

Y92659-63 are mutant immunogenised murine prostate specific membrane antigen (PSM) constructs, which contain a foreign epitope, p10. The PSM can be used to identify whether autoantibodies to mouse PSM can be broken down by the use of protease inhibitors. Autoantibodies to PSM can be used as a marker for disease progression. Immunogenic analogues of PSM can be used in mice by PSM analogues. Immunogenic analogues of PSM can be used in the claimed method as an autovaccine to induce a CTL response. The method is used for inducing immune responses against weakly immunogenic tumours such as prostate cancer. The method is used for inducing immune responses against weakly immunogenic cancers (cell-proliferating), e.g. melanoma, colorectal cancer, lung cancer, fibrosarcoma, glioblastoma, neuroblastoma, osteosarcoma, rhabdomyosarcoma, fibroblast growth factor b (FGFB). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T lymphocyte) associated epitope from a group of CTL epitopes derived from the cell-associated PA; and (2) at least 1 CTL epitope from the PA and foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGFB comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one CTL epitope from the PA and one CTL epitope from the PA used to treat prostatic, prostatic/breast or breast cancer when the PA is human PSM, FGFB and Her2, respectively.

Note: This sequence was constructed from the murine PSM splice variant (Y92659-7), which appears on pages 210-213 of the specification.

XX	Key	Location/Qualifiers
PH	Peptide	631, 651
PT		/label= p90
XX		
XX		
PN		WC200020027-A2
XX		
PD	13-APR-2000.	
XX		
PD	05-OCT-1999.	99MO-DK00525.
XX		
PR	05-OCT-1998.	98DK-0001261.
PR	20-OCT-1998.	98OS-0105011.
XX		
PA	(HEB-) M & E BIOTEC MS.	
XX		
PI	Steinaa L, Mouritzen S, Nielsen KG, Haaning J, Leach D, Dalum I;	
PI	Gautam A, Blir P, Karlsson G.	
DR		
DR	WPI: 2000-349937/30.	
PT		

	Query Match	5.1%	Score 36;	DB 21;	Length 698;
	Best Local Similarity	100.0%	Pred No 1.4e-28;		
	Matches	36;	Conservative	0;	Mismatches 0;
				Indels	0;
	Caps	0;			
D6	395 SLLGLRQVAVYINLADSLSGYTLIVDCPLHYALV 430				
	387 SLLIGRYVAYINLADSLSGYTLIVDCPLHYALV 422				
RESULT 34					
V92662					
ID	Y92662 standard; Protein; 703 AA.				
AC	Y92662;				
XX					
D7	10-AUG-2000 (first entry)				
D8					
XX	Mutant murine PSM splice variant construct, mPSM.Y.				
XX					
FN	Prostate specific membrane antigen; splice variant; mutant;				
FN	vaccination; cytotoxic T-lymphocyte immunity; breast cancer;				
XX	prostate cancer; cell-associated peptide antigen; foreign epitope.				
XX					
O5	Mus musculus.				
	Synthetic.				

Y9368-63 are mutant immunogenized murine foreign specific membrane antigens (PSM) constructs which contain a foreign epitope, 730. The antigen can be used to study whether auto tolerance to mouse PSM can be broken by immunization and/or DNA vaccination against murine PSM. This method is also useful to study the mechanism of self tolerance and the claimed method as an adjuvant to induce a CTL response. The method is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA), such as those associated with fibrosarcoma, B-cell lymphoma, melanoma, K. (test2) and/or glioblastoma multiforme. By immunizing mice with a mixture of a PSM and a simultaneously presented by antigen producing cells (APCs) of the animal immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the antigen and (2) antibody against murine PSM, antibodies are formed against the antigen and (3) antibody against murine PSM. These antibodies form part of the human/murine IgGmB comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope or also claimed. The method is used for PSA, RGDH and HLA-2 resistant viral and bacterial antigens and cancer. Note: This sequence was published on pages 210-213 of the murine PSM application (Y93624), which appears on pages 210-213 of the specification.

Sequence 703.MA.

Query Match 5.18; Score 36; DB 21; Length 703;
Best Local Similarity 100.0%; Pred. No. 1.5e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 395 SELLGRCVATVIMADSTIEGWTATVDCPTPLATSLV 430
DB 393 atllqeyvaylnadaieqnyllvtocpplayaly 418
Y92659
ID Y92659 standard: Protein: 752 AA.
AC Y92659:
XX 10-NOV-2000 (first entry)
XX Murine prostate specific membrane antigen.
DE Murine prostate specific membrane antigen; apply variant: vaccination;
KW cytotoxic T-lymphocyte immunity; self-protein; foreign epitope;
RW prostate cancer; cell-associated peptide antigen; foreign epitope;
OS Mus musculus.
XX M0200020027-A2.
XX 13-APR-2000.
XX 05-OCT-1999; 99MO-DK00525.
XX 05-OCT-1998; 98DK-0001261.
XX 20-OCT-1998; 98OS-0105011.
XX (MEB1-) M & E BIOTECH AS.
PI Stelaia L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;
PI Gautam A, Birk P, Karlsson G;
DR WPI: 2000-349317/30.
DR N-PSDB: A09458.
XX Inducing immune responses to weakly immunogenic, tumor associated
PT peptide antigens for the treatment of breast and prostate cancer
XX Example 1: Page 204-206; 220pp; English.
XX The claims detail a method for inducing immune responses against weakly
CC immunogenic, tumor associated peptide antigens (i.e. self-proteins), for example, human
CC associated with cancers (i.e. self-proteins), for example, human

XX 05-OCT-1998; 98DK-0001261.
XX 20-OCT-1998; 98OS-0105011.
XX (MEB1-) M & E BIOTECH AS.
PI Stelaia L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;
PI Gautam A, Birk P, Karlsson G;
DR WPI: 2000-349317/30.
XX Inducing immune responses to weakly immunogenic, tumor associated
PT peptide antigens for the treatment of breast and prostate cancer
XX Example 1: Page 204-206; 220pp; English.
XX Y92659-62 are mutant immunogenized murine prostate specific membrane
CC antigen (PSM) constructs, which contain a foreign epitope, P30. The
CC broken in mice by immunization and/or DNA vaccination against murine PSM
CC using murine PSM analogues. Immunogenic analogues of PSM can be used in
CC the claimed method as an autovaccine to induce a CTL response. The
CC cell-associated peptide antigens (PA) such as those associated with
CC cancers (self-proteins), e.g. human PSM, heregulin 2 (Hr2) and/or
CC fibroblast growth factor 8b (FGF8b). The method comprises effecting
CC an animal immune system of (1) at least 1 CTL (cytotoxic T-lymphocyte)
CC group derived from the PA and/or at least 1 B-cell group derived from the
CC cell-associated PA; and (2) at least 1 first T helper cell group which is
CC foreign to the animal. Analogues of human PSM, human Hr2 and
CC human FGF8b are used as the PA and/or the cell-associated PA. The
CC predicted CTL and B-cell epitopes of the respective PA and including at
CC least one foreign T helper epitope are also claimed. The method is used
CC to treat prostate, prostate/breast or breast cancer when the PA is human
CC Note: This sequence was constructed from the wild type murine PSM
CC (Y92623), which appears on pages 204-206 of the specification.
XX Sequence 756 AA:

Query Match 5.18; Score 36; DB 21; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.5e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 395 SELLGRCVATVIMADSTIEGWTATVDCPTPLATSLV 430
DB 445 atllqeyvaylnadaieqnyllvtocpplayaly 480

CC prostate specific membrane antigen (PSM), heregulin 2 (Hr2) and/or
CC fibroblast growth factor 8b (FGF8b). The method comprises effecting
CC an animal immune system of (1) at least 1 CTL (cytotoxic T-lymphocyte)
CC group derived from the PA and/or at least 1 B-cell group derived from the
CC cell-associated PA; and (2) at least 1 first T helper cell group which is
CC foreign to the animal. Analogues of human PSM, human Hr2 and
CC human FGF8b are used as the PA and/or the cell-associated PA. The
CC predicted CTL and B-cell epitopes of the respective PA and including at
CC least one foreign T helper epitope are also claimed. The method is used
CC to treat prostate, prostate/breast or breast cancer when the PA is human
CC PSM, Hr2b and Hr2c, respectively.
XX Sequence 752 AA:
QY 395 SELLGRCVATVIMADSTIEGWTATVDCPTPLATSLV 430
DB 441 atllqeyvaylnadaieqnyllvtocpplayaly 476
Y92659
ID Y92659 standard: Protein: 756 AA.
AC Y92659:
XX 10-NOV-2000 (first entry)
XX Murine prostate specific membrane antigen construct, mPSMK.
DE Murine prostate specific membrane antigen; immunogenized construct; mutant;
KW vaccination; cytotoxic T-lymphocyte immunity; breast cancer;
RW prostate cancer; cell-associated peptide antigen; foreign epitope;
XX Mus musculus.
XX Synthetic.
XX Key Location/Qualifiers
FT Peptide 255..275
FT /Label= P30
XX M0200020027-A2.
XX 13-APR-2000.
XX 05-OCT-1999; 99MO-DK00525.

RESULT 37
Y92660
ID Y92660 standard: Protein: 761 AA.
AC Y92660:
XX 10-NOV-2000 (first entry)
XX Murine prostate specific membrane antigen construct, mPSMT.
DE Murine prostate specific membrane antigen; immunogenized construct; mutant;
KW vaccination; cytotoxic T-lymphocyte immunity; breast cancer;
RW prostate cancer; cell-associated peptide antigen; foreign epitope;
XX Mus musculus.
XX Synthetic.
XX Key Location/Qualifiers
FT Peptide 689..709
FT /Label= P30
XX M0200020027-A2.
XX 13-APR-2000.
XX 05-OCT-1999; 99MO-DK00525.
XX 05-OCT-1998; 98DK-0001261.
XX 20-OCT-1998; 98OS-0105011.
XX (MEB1-) M & E BIOTECH AS.
PI Stelaia L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;
PI Gautam A, Birk P, Karlsson G;
DR WPI: 2000-349317/30.
XX Inducing immune responses to weakly immunogenic, tumor associated
PT peptide antigens for the treatment of breast and prostate cancer
XX Example 1: Page 220pp; English.
XX Y92659-62 are mutant immunogenized murine prostate specific membrane
CC antigen (PSM) constructs, which contain a foreign epitope, P30. The
CC broken in mice by immunization and/or DNA vaccination against murine PSM
CC using murine PSM analogues. Immunogenic analogues of PSM can be used in
CC the claimed method as an autovaccine to induce a CTL response. The
CC method is used for inducing immune responses against weakly immunogenic
CC peptide antigens (i.e. self-proteins), e.g. human PSM, heregulin 2 (Hr2) and/or
CC cancers (self-proteins), e.g. human PSM, heregulin 2 (Hr2) and/or

PA (SLOAN) SLOAN KETTERING INST CANCER RES.
 PI PAIR NR, Heaton MDM, Israeli RS.
 XX WPI: 1996-402365/40.
 DR WPI: 1996-402365/40.
 XX DNA encoding alternative applied prostate-specific membrane
 PT antigen (PSM) developed by Sloan Kettering Institute for
 PT micrometastatic tumour cells, or prostate cancer progression
 PS Example 1: Page 49: 284pp: English.
 CC Trypatic peptides (M02237-45) were chid from the human prostate-
 CC specific membrane (PSM) antigen (see also M02234) and used to
 CC design primers (736795-808) utilized in the isolation of a cDNA
 CC clone (736795) coding for PSM. The isolated cDNA and PSM protein
 CC were used to design primers for the diagnosis and treatment
 CC of prostate cancer and metastasis.
 XX Sequence 19 AA:
 S0
 Query Match 2.7%: Score 19: DB 17: Length 19:
 Best Local Similarity 100.0%: Pred. No. 2,3e-12:
 Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 656 YAGSPPTATLADPFRK 674
 Db 1 YAGSPPTATLADPFRK 19
 RESULT 41
 M45408 ID M45408 standard: Peptide: 18 AA.
 XX M45408:
 DT 06-JUL-1998 (first entry)
 XX PMSA peptide (aa196-213) peptide 6.
 XX Prostate-specific glandular kallikrein: hK2 protein: human:
 KW Prostate-specific antigen; PSM; prostate carcinoma;
 KW Prostate cancer; Benign prostatic hyperplasia; diagnosis; PMSA.
 OS Synthetic.
 XX Key Location/Qualifiers
 PH Cleavage-site 9..10
 PT Cleavage-site 14..15
 PT Cleavage-site 14..15

R55102 ID R55102 standard: Peptide: 22 AA.
 XX R55102:
 DT 11-JAN-1995 (first entry)
 XX Prostate-specific membrane antigen peptide fragment.
 XX Prostate-specific membrane antigen; PSM; prostate cancer;
 KW transmembrane glycoprotein; imaging; targeting; tumour detection;
 KW antibody detection; sequencing.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 PH Miso-difference 4 /note= "unidentified residue"
 PT Miso-difference 4 /note= "unidentified residue"
 PT M09409820-A.
 XX M09409820-A.
 PD 11-MAY-1994.
 XX 05-NOV-1993: 93MO-0510624.
 XX 05-NOV-1992: 93DS-0973337.
 PR (SLOAN) SLOAN KETTERING INST CANCER.
 PA PAIR NR, Heaton MDM, Israeli RS.
 XX WPI: 1994-167129/20.
 DR WPI: 1994-167129/20.
 XX Prostate-specific membrane antigen and DNA encoding it - 1a
 PT useful for detecting hematogenous micro-metastatic tumour cells
 PT and for identifying ligands which bind to PSM Ag
 XX Example : Page 46: 196pp: English.
 CC The inventors attempted to sequence the PSM Ag by modified Edman
 CC degradation. Peptides (855098-107) that gave clear dominant peaks
 CC on HPLC from the digested PSM Ag sample were used. Some of the
 CC peptides were identified by mass spectrometry. Some of these
 CC levels and identified with lower confidence. Some of these peptides
 CC were used to design primers to carry out PCR to identify cDNA clones
 CC encoding the PSM Ag. R55102 was used to design primers G65377-30.
 CC A cDNA clone (736795) was identified as part of the PSM sequence
 CC encoding the PSM Ag. The PSM Ag was identified as part of the
 CC by G65377-30. The PSM coding sequence is useful for suppressing or

PT Cleavage-site 13..16
 PT /note= "hK2 cleavage site"
 XX M09802748-A1.
 XX M09802748-A1.
 XX 22-JAN-1998.
 XX 15-JUL-1997: 97MO-0512322.
 XX 15-JUL-1996: 96DS-0680868.
 PR (HYBR-) HYBRITRCH INC.
 PA (MAYO-) MAYO FOUNDATION.
 PI Grauer L, Klee GG, Mikolajczyk SD, Saeed M, Tindall DJ.
 XX Young CIP.
 DR WPI: 1996-120376/11.
 XX Diagnostic methods using antibodies which bind prostate antigens -
 XX for c.g. monitoring treatment or progression of prostate
 XX cancer
 XX Example 7: Fig 16: 100pp: English.
 XX Peptide 6 represents amino acid residues 196-213 of PMSA.
 CC Peptides 1-6 (see M45402 and M45404-08) were used as substrates to
 CC the examine amidolytic activity of prostate specific antigen (PSA)
 CC hK3 (see M45398) and of prostate-specific glandular kallikrein hK2
 CC (see M45397). All peptides tested hK2 had specificity only for 2
 CC selected arginines, and PSA primarily for selected tyrosine,
 CC phenylalanine and leucine residues. The invention provides
 CC diagnostic methods using antibodies which bind prostate antigens
 CC for c.g. monitoring the treatment or
 CC progression of prostate cancer.
 XX Sequence 18 AA:
 S0
 Query Match 2.5%: Score 18: DB 19: Length 18:
 Best Local Similarity 100.0%: Pred. No. 2,4e-11:
 Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 152 CCRGIVAKRGVPRNKK 169
 Db 1 CCRGIVAKRGVPRNKK 18
 RESULT 42

CC modulating the metastatic ability of prostate tumour cells to grow,
 CC or for eliminating them. The protein is useful to identify or purify
 CC ligands of the Ag and is also useful for the diagnosis of prostate
 CC imaging and targeting of prostate tumour deposits.
 XX Sequence 22 AA:
 S0
 Query Match 2.4%: Score 17: DB 15: Length 22:
 Best Local Similarity 100.0%: Pred. No. 3,1e-10:
 Matches 17: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 34 TQPHNACRQNRQAK 50
 Db 6 TQPHNACRQNRQAK 22
 RESULT 43
 M02241 ID M02241 standard: Peptide: 22 AA.
 XX M02241:
 DT 05-NOV-1996 (first entry)
 XX Prostate-specific membrane antigen peptide 2734 6.
 XX Prostate-specific membrane antigen; PSM; prostate cancer;
 KW metastasis; therapy; diagnosis.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 PH Miso-difference 4 /note= "unidentified amino acid"
 PT Miso-difference 5 /note= "unidentified amino acid"
 PT M09626272-A1.
 XX M09626272-A1.
 PD 29-AUG-1996.
 XX 23-FEB-1996: 96MO-0502424.
 XX 03-JUN-1995: 95DS-0470735.
 XX 24-FEB-1995: 95DS-0394157.
 PR 03-JUN-1995: 95DS-0466381.
 XX (SLOAN) SLOAN KETTERING INST CANCER RES.
 PA PAIR NR, Heaton MDM, Israeli RS;

XX WP1: 1996-402365/40.
 XX DNA encoding alternatively spliced prostate-specific membrane
 PT antigen - useful to develop prods. for detecting haematogenous
 XX micrometastatic tumour cells, or prostate cancer progression
 XX Example 1: Page 49: 284pp: English.
 XX Tryptic peptides (W0237-45) were obtd. from the human prostate-
 CC specific membrane (PSM) antigen (see also W0234) and used to
 CC design primers (736795-808) utilised in the isolation of a cDNA
 CC clone (736785) coding for PSM: primers 1-L (736801-04) are
 CC based on amino acids 14-19 of peptide 2734 6 (W0234). The
 CC isolated cDNA and PSM protein are useful in developing methods for
 CC the diagnosis and treatment of prostate cancer and metastasis.
 XX Sequence 22 AA:
 50
 Query Match 2.1%; Score 17; DB 17; Length 22;
 Best Local Similarity 100.0%; Pred. No. 3.1e-10;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 34 AFDPGLDLPDPPYR 50
 Db 6 EQPHLPGTEQNGDLAK 22
 RESULT 44
 R55105
 ID R55105 standard; Peptide: 15 AA.
 XX R55105;
 XX 11-JAN-1995 (first entry)
 DT
 XX Prostate-specific membrane antigen peptide fragment.
 XX Prostate-specific membrane antigen; PSM: prostate cancer;
 KW transmembrane glycoprotein; Imaging: targeting; tumour detection;
 KW antibody detection; sequencing.
 XX Homo sapiens.
 XX M09409820-A.
 XX 11-MAY-1994.
 XX 05-NOV-1993; 93WO-0810624.
 XX

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KW metastasis; therapy; diagnosis.
 XX Homo sapiens.
 XX M09626272-A1.
 XX 29-AUG-1996.
 XX
 XX 23-FEB-1996; 96WO-0802424.
 XX 02-JUN-1995; 95US-0410735.
 XX 24-FEB-1995; 95US-0394152.
 XX 02-JUN-1995; 95US-0466381.
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 XX Fair WR, Heaton MDM, Israeli RS;
 PI MPI: 1996-402365/40.
 XX DNA encoding alternatively spliced prostate-specific membrane
 PT antigen - useful to develop prods. for detecting haematogenous
 XX micrometastatic tumour cells, or prostate cancer progression
 XX Example 1: Page 49: 284pp: English.
 XX Tryptic peptides (W0237-45) were obtd. from the human prostate-
 CC specific membrane (PSM) antigen (see also W0234) and used to
 CC design primers (736795-808) utilised in the isolation of a cDNA
 CC clone (736785) coding for PSM: primers 1-L (736801-04) are
 CC based on amino acids 14-19 of peptide 2734 6 (W0234). The
 CC isolated cDNA and PSM protein are useful in developing methods for
 CC the diagnosis and treatment of prostate cancer and metastasis.
 XX Sequence 15 AA:
 50
 Query Match 2.1%; Score 15; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 630 AFDPGLDLPDPPYR 644
 Db 1 ATIDPLSLDPPYR 15
 RESULT 46
 Y30346
 ID Y30346 standard; peptide: 16 AA.
 XX Y30346;
 XX

XX 05-NOV-1992; 92US-0973337.
 XX (SLOK) SLOAN KETTERING INST CANCER.
 XX Fair WR, Heaton MDM, Israeli RS;
 XX MPI: 1994-167129/20.
 XX Prostate-specific membrane antigen and DNA encoding it - is
 PT useful for detecting haematogenous micro-metastatic tumour cells
 PT and for identifying ligands which bind to PSM Ag
 XX Example 1: Page 44: 196pp: English.
 XX The inventors attempted to sequence the PSM Ag by modified Edman
 CC degradation. Peptides (455098-107) that gave clear dominant peaks
 CC were identified. Some of these peptides were present in very low
 CC levels and identified with lower confidence. Some of these peptides
 CC were used to design primers to carry out PCR to identify cDNA clones
 CC encoding the PSM Ag. A clone, 1R-20 was identified as a partial PSM
 CC antigen. The PSM Ag was sequenced by Edman degradation and
 CC by G55520). The PSM coding sequence is useful for suppressing or
 CC modulating the metastatic ability of prostate tumour cells to grow,
 CC or for eliminating them. The protein is useful to identify or purify
 CC antibodies that bind to the antigen. The protein is also a tumour target for Ab-directed
 CC imaging and targeting of prostatic tumour deposits.
 XX Sequence 15 AA:
 50
 Query Match 2.1%; Score 15; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 630 AFDPGLDLPDPPYR 644
 Db 1 ATIDPLSLDPPYR 15
 RESULT 45
 W02243
 ID W02243 standard; Peptide: 15 AA.
 XX W02243;
 XX 05-NOV-1996 (first entry)
 DT
 XX Prostate-specific membrane antigen peptide 2738 1.
 XX Prostate-specific membrane antigen; PSM: prostate cancer;
 KW

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DT 15-NOV-1999 (first entry)
 XX N-terminal sequence of the PSM' protein.
 XX PSM' protein; splice variant; prostate specific membrane antigen;
 KW cancer marker; prostatic cancer.
 XX Synthesis
 XX Homo sapiens.
 XX M09943710-A1.
 XX 02-SEP-1999.
 XX 22-FEB-1999; 99WO-0803810.
 XX 26-FEB-1998; 98US-0011220.
 XX (BEC-) BECTMAN COUTZER INC.
 XX Grauer US, Kuus-Retchel K, Sokoloff R;
 PI MPI: 1999-540563/45.
 XX New PSM' protein, splice variant of prostate-specific membrane
 PT antigen, used as marker for prostatic cancer for diagnosis,
 XX prognosis and treatment
 XX Claim 22: Page 39: 52pp: English.
 XX The present sequence is derived from the N-terminal of the PSM' protein,
 CC which is identified by a PCR method. The present sequence can be used to
 CC raise monoclonal antibodies. Detection of PSM' in a sample, particularly
 CC using specific antibodies, is useful for diagnosis of prostate cancer.
 CC Biotinylated antibodies, injected into the prostate gland, are useful
 CC for diagnosis. Antibodies may also be coupled to therapeutic agents, such as
 CC drugs, toxins, etc., and used to treat prostate cancer.
 XX Sequence 16 AA:
 50
 Query Match 2.1%; Score 15; DB 20; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.7e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 16 AFDELEAMNKKFL 30
 Db 1 ATIDELAMNKKFL 15

